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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                             121 NRIELKGMDFKEDGNILGHKLEYNFNSHNVYIMPDKANNGLKVNFKIRHNIEGGGVQLAD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M., Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aeguorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M., Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aequorea macrodactyla.
Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                83.7%; Score 1059; DB 5; Length 238; ilarity 80.7%; Pred. No. 3.4e-83; Conservative 18; Mismatches 28; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
83.6%; Score 1057; DB 5; Length 238;
Best Local Similarity 81.5%; Pred. No. Se-83;
Matches 194; Conservative 15; Mismatches 29; Indels
                                                                               Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435430; AAL33915.1; --
EMBL; AF435430; AAL33915.1; --
EO, GO.006091; Prenergy pathways; IEA.
InterPro; IPR009017; GFP_Ilke.
InterPro; IPR0090786; Green_fil_protein.
Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUCNESCENT.
PRODOM; P013756; Green_fil_protein; 1.
PRODOM; P013756; Green_fil_protein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databages.
EMBL, AF435432; AAL33917.1; -.
GO; GO:0006691; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR009786; Green_fl_protein.
Pf01353; GFP; II
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ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27018 MW; 75521EA5534E573A CRC64;
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Last annotation update)
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Best Local Similarity
Matches 192; Conserv
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                                                                        macrodactyla.";
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1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL

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121 NRIELKGMDFKEDGNILGHKLEYNFNSHNVYIMPDKANNGLKVNFKIRHNIEGGGVQLAD 180
                                                                                61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 EDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITH 231
1 MSKGEELFTGVVPILVELDGDVAGHKFSVRGEGEGDADYGKLEIKFICTTGKLPVPWPTL 60
                                                                                                                                                                                                                                                                                            181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
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Wakaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
Faviina; Faviidae; Montastraea.
NCBI_TaxID=63558;
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; Pred. No. 2.4e-13;
46; Mismatches 71; Indels 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Falkowski P.G., Sun Y.;
Falkowski P.G., Sun Y.;
Montastraea cavernosa fluorescent protein.";
Submitted (SEP-2001) to the EMBL/Genbank/DDBJ databases.
EMBL; AY056460; AAL17905.1;
CO:0006091; Penergy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR0090786; Green_fl_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 AA; 25775 MW; 52DE2F716D083524 CRC64;
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PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl_protein; 1.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
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25.9%;
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Best Local Similarity
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NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                       61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 120
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                                                             181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                            HYQTNVPLGDGPVLIPINHYLSFQTAISKDRNETRDHMVFLBFFSACGHTHGMDELYK 238
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Aeguoreidae; Aeguorea.
NCBI_TaxID=147615;
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.9%; Score 1061; DB 5; Length 238; larity 80.7%; Pred. No. 2.3e-83; Conservative 18; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                              macrodactyla..;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; AF495-428; AAL33913.1;
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR00917; GFP like.
InterPro; IPR000916; Green_fl_protein.
Pfan; PF01353; GFP; I.
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ProDom; PD013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 27031 MM; 5F80A19C19DC584D CRC64;
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Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20,
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192;
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Matches
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Q8WTC7
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Ebkaryota; Metazoa; Gnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q.,
Li S.J., Xia N.S.,
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                         Length 238;
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; AR435429; AAD33914.1; -.
GO; GO: 0006691; P: energy pathways; IEA.
InterPro; IPR003017; GFP_like.
InterPro; IPR003017; GFP_like.
Pfam; PF01153; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl_protein; 1.
SEQUENCE 238 AA; 27047 WW; 5F80Al8FALE7C84D CRC64;
(OCT-2001) to the EMBL/GenBank/DDBJ databases.
       Last sequence update)
Last annotation update)
                                                                                                                                                                 28;
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80.7%; Pred. No. 2.3e-83;
tive 18; Mismatches 28;
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                                                                                                                                     84.0%; Score 1062; DB 5;
80.7%; Pred. No. 1.9e-83;
ive 18; Mismatches 28
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Green fluorescent protein,
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Matches 192, Conservative
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                                                                                                                                     Query Match
Best Local Similarity
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01-MAR-2002
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Best Local
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                                                                                                                                                                                                                                                                                    Green fluorescent protein
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                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                  (TrEMBLrel.) (TrEMBLrel)
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                                                                                                                                                                                             (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                   Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Q8WTC4;
01-MAR-2002 (
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Bukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                                                      Length 238;
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Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
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84.7%; Score 1072; DB 5; Length 238;
Best Local Similarity 81.5%; Pred. No. 2.6e-84;
Matches 194; Conservative 18; Mismatches 26; Indels
                                                                                                                                                              25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF415431; AAL33916.1; -
GO, GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR0090786; Green_fl_protein.
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PRINTS; PR01229; GFLUCRESCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27015 MW; 6B8FD75E88926903 CRC64;
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27049 MW; 8185D0E5E529012B CRC64;
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Last annotation update)
                                                                                             85.2%; Score 1078; DB 5;
81.9%; Pred. No. 7.8e-85;
ive 18; Mismatches 25;
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01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                           Conservative
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                                                                                                                         Best Local Similarity
Matches 195; Conserv
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Q8WTC6;
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61 VTLGYGILCFARYPEHMKMNDFFKSAMPEGYIQERTIFFQDDGKYKTRGEVKFEGDILV 120
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.,
"Colorful mutants of green fluorescent protein from Aequorea
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
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EMBL, AF435431, AAL33918 11, -...
GO: GO: 0006091; P: energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR000766; Green fl_protein.
Pfam; PF01325; GFP; 1...
PRINTS; PR01229; GFLUORESCENT.
PROMOM; P013756; Green fl_protein; 1.
SEQUENCE 238 AA; 26956 MW; 75521EAF0CEBA73A CRC64;
                                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
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81.9%; Pred. No. 1.2e-83;
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238
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SEQUENCE
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Eukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 238;
Pred. No. 1.1e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1] — SEQUENCE FROM N.A. Matching J.K.; Matching J.N., Campbell A.K.; Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases. EMBL; X83959; CAAS8789.1; -. PIR; JS0692; JQ1514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 AA; 26950 MW; 26E2BE450E748E44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  017105 PRELIMINARY, PRT; 238 AA.
017105;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.2%; Score 1192; DB 5;
92.9%; Pred. No. 1.2e-94;
live 7; Mismatches 10;
                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, P42212; IGFL.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR00786; Green_fl_protein.
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PRINTS; PR01229; GFLUORESCENT.
ProDom, PD013756; Green fl protein; 1.
                    96.2%;
                                     229; Conservative
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                    Similarity
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es 221;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                  Best Local
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Q17106
ID Q17106
                                     Matches
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238 AA

PRT;

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                                                                                                             Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
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Eukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                                                                                                                                                                                                                                                                                                                                                      93.4%; Score 1181; DB 5; Length 238; 92.4%; Pred. No. 1e-93; ive 7; Mismatches 11; Indels
                                                                                                                                                                     SEQUENCE FROM N.A. Watkins J.M., Campbell A.K.; Watkins J.M., Campbell A.K.; Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases. EMBL, X83960; CAA58790.1; -. PIR; JS0662; JQ1514.
                                                                                                                                                                                                                                                                                                                                                                         238 AA; 26867 MW; BD4648262D8EABD4 CRC64;
Q17106;
01-NOV-1996 (TrEWBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein (Fragment).
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Last sequence update)
Last annotation update)
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GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green fl protein.
                                                                                                                                                                                                                                                                                                       Pfan, PF01353, GFP, 1.
PRINTS; PR01229, GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
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                                                                                           Aequorea victoria (Jellyfish)
Eukaryota; Metazoa; Cnidaria;
Aequoreidae; Aequorea.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 92.4
Matches 220, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                          NCBI_TaxID=6100;
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Q8WP95;
01-MAR-2002 (
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                         NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKOKNGIKANFKIRHNIEDGSVOLAD 180
                                                                                                                  NRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
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                                                                                                                                                                           181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                              181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLEFVTAAGITHGMDELYK 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koranyi P., Berenyi M., Burg K.;
"Occurrence of green fluorescence protein in diazotrophic bacteria
Azomonas and Azotobacter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
NCBL TaxID=354;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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97.1%; Pred. No. 3.5e-98;
ative 1; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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(TrEMBLrel. 23, I
(TrEMBLrel. 25, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                      UL-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Green fluorescence protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonadaceae; Azomonas.
NCBI_TaxID=116849;
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01-OCT-2003
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Q8GHE4;
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Koranyi P., Berenyi M., Burg K.,
"Occurrence of green fluorescence protein in diazotrophic bacteria
Azononas and Azotobacter.",
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF324406, AAN86138.1, -.
EMBL, AF324406, Penergy pathways; IEA.
InterPro, IPR009017; GFP_like.
InterPro, IPR009017; GFP_like.
InterPro, IPR009017; GFP_like.
FF01353; GFP; 1.
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MEDLINE=96305137; PubMed=8707053;
Cormack B.P., Valdivia R.H., Falkow S.;
"FACS-optimized mutants of the green fluorescent protein (GFP).";
Gene 173:33-38(1996).
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Cormack B.P., Bertram G., Egerton M., Gow N.A.R., Falkow S.,
Brown A.J.P.;
Wrast Enhanced Green Fluorescent Protein (yEGFP): a reporter of expression in Candida albicans.";
Microbiology 0:0-0(1996).
EMBL, 073901; AABR
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Aequoreidae; Aequorea.
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                                                                                                                                                                                                                                                                                                                                             97.4%; Score 1232; DB 2; Length 2 97.1%; Pred. No. 4.3e-98; ive 1; Mismatches 6; Indels
                                                                                                                                                                                                                               PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26887 MW; E0E1616BD2AF6188 CRC64;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green_fl_protein.
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Matches 231; Conservative
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April 19, 2004, 15:02:40; Search time 45 Seconds (without alignments) 1668.741 Million cell updates/sec
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1265
1 MSKGEELFTGVVPILVELDG......VLLEFVTAAGITHGMDELYK 238
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                        1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
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2: sp_bacteria:*
3: sp_fung:*
4: sp_human:*
5: sp_invertebrate:*
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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1	OBGHE2 PRELIMINARY; PRT; 238 AA. OBGHE2;	01-MAR-2003 (TrEMBLrel. 23, Created)	(TrEMBLrel, 23,			2289GFP.	Azotobacter vinelandii.	Bacteria; Proteobactería; Gammaproteobacteria: Pseudomonadales.	Pseudomonadaceae; Azotobacter.	NCBI_TaxID=354;		SEQUENCE FROM N.A.	STRAIN=DSM2289;	Koranyi P., Berenyi M., Burg K.;	"Occurrence of green fluorescence protein in diazotrophic bacteria	Azomonas and Azotobacter.";	Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.	EMBL; AF324408; AAN86140.1;	; GO:0006091; P:energy pathways; IEA.	InterPro; IPR009017; GFP_like.	InterPro; 1PR000786; Green fl protein.	Pfam; PF01353; GFP; 1.	PRINTS; PR01229; GFLUORESCENT.	u	DUENCE 238 AA; 26914 MW; F84840F1F9064018 CRC64;	97.98;	il Similarity 97.5%; Pred. No. 1.3e-98;	232; Conservative 1; Mismatches 5; Indels 0; Gaps	SVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL	MSKGRFI FTGIATOTTATE TODANACUVECATE THE STATE	TOTAL THE TRANSPORT TO THE TRANSPORT TO THE TOTAL TO THE
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April 19, 2004, 15:04:50 ; Search time 22 Seconds (without alignments) 558.499 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1265 1 MSKGEELFTGVVPILVELDG......VLLEFVTAAGITHGMDELYK 238 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

389414 Total number of hits satisfying chosen parameters: 389414 seqs, 51625971 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:*
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6: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		ID	US-08-753-143-2	-08-679-865-	-08-680-87	-08-792-553-	-08-753-144-	-09-094-359-	-09-172-063-	-09-263-975-	-08-727-452-	-09-418-785-	-09-129	-09-129	-09-602-641-2	-09-704-463-	-08-893-327-	08-337-915A	-09-121-539-1	-09-214-909-	-09-479-645A	-09-479-645A-1	-09-472-065A-4	- 1	_	S-09-023-946B-	-08-646-539-2	00-640-000-	2-22-505-60-	US-09-472-065A-2
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APPLICANT: Tsien, Roger Y.
APPLICANT: Cubit, Andrew B.
TITLE OF INVENTION: Assays for Protein Kinases Using
TITLE OF INVENTION: Fluorescent Protein Substrates
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:

US-08-679-865-2; Sequence 2, Application US/08679865; Patent No. 5912137; GENERAL INFORMATION:

Sequence 94. Appl	Semience 96 Appl	Semience 98 April		200	Semience 104 App	110	2 4	in	Segments of Applications	ic	, c	Semience 2, Appil	Seguence 80, Appl	, ,	32, A	Sequence 148, App	150	Sequence 152, App
US-09-479-645A-94	US-09-479-645A-96	US-09-479-645A-98	US-09-479-645A-100	US-09-479-645A-102	US-09-479-645A-104	US-09-479-645A-110	US-09-091-042A-2	US-09-127-227-2	US-08-588-201-2	US-09-169-605-2	US-08-893-327-2	US-09-479-645A-88	US-09-479-645b-90	11S-09-479-645h-02	26-WCF0 67F 60 GE	US-09-479-645A-148	US-09-479-645A-150	US-09-479-645A-152
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28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	7	44	45

ALIGNMENTS

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61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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Indels
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Pred. No. 6.8e-127;
1; Mismatches 5;
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Best Local Similarity 97.5%;
Matches 232; Conservative
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; ORGANISM: Aequorea victoria
US-08-753-143-2
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LENGTH: 238
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TELEFAX: 619-678-5099 INFORMATION FOR SEQ ID NO:
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STATE: Ca
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APPLICANT: Tsien, Roger Y.
APPLICANT: Cubitt, Andrew B.
TITLE OF INVENTION: Assays for Protein Kinases Using TITLE OF INVENTION: Fluorescent Protein Substrates NUMBER OF SEQUENCES: 48
                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/679,865 FILING DATE: 16-JUL-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patentin Release #1.0, Version #1.30
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ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
3: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                          02307Z-069000
                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTELLA, JOHN S.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 02307
TELEPHONE: (415) 576-0200
INFORMATION: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Patent No. 5925558
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 238 amino acids
amino acid
                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-679-865-2
          STREET: Two Dances CITY: San Francisco
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SOFTWARE: PatentI
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                                                                        COUNTRY: USA
ZIP: 94111-3834
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Best Local Similarity
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; Patent No. 5981200
; GENERAL INFORMATION:
; APPLICANT: Heim, Roger Y.
APPLICANT: Heim, Roger
; TITLE OF INVENTION: Tandem Fluorescent Protein Constructs
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: Las Jolla
; STAME: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.9%; Score 1238; DB 2; Length 238; 97.5%; Pred. No. 6.8e-127; ive 1; Mismatches 5; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,553
FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,876
FILING DATE: 16-UTL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John S.
REGISTATION NUMBER: 32,94
REFERENCE/DOCKET NUMBER: 02307Z-069;
TELECOMMUNICATION INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
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.....IERISTICS:
TYPE: amino acid
TOPOLOGY: 1:--
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-680-876-2
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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97.9%;
97.5%;
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Best Local Similarity 97.5%;
Matches 232; Conservative
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                                     Query Match
Best Local Similarity 97.5
Matches 232; Conservative
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TYPE: PRT
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        US-08-753-144-2
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US-09-172-063-2
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Patent No. 606476
GENERAL INFORMATION:
APPLICANT: Heim, Roger Y.
APPLICANT: Heim, Roger
TITLE OF INVENTION: MODIFIED GREEN FLUORESCENT PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                            Score 1238; DB 2;
Pred. No. 6.8e-127;
1; Mismatches 5;
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OPERATING SYSTEM: Windiws95
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,144
FILING DATE: 20-NOV-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla STREET CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38,347
ER: 07257/032002
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APPLICATION NUMBER: 08/727,452
FILING DATE: 10-007-1996
APPLICATION NUMBER: USS5/14692
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: 08/337,915
FILING DATE: 10-NOV-1994
ATTOREY/ABENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 07.257/02
TELECOMMUNICATION INPORMATION:
TELEPRONE: 109/678-5070
TELEFRAX: 619/678-5070
TELEFRAX: 619/678-5070
TELEFRAX: 619/678-5070
TELEFRAX: 019/678-5070
                                                                                                            97.98;
             238 amino acids
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amino acid
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Matches 232; Conservative
SEQUENCE CHARACTERISTICS
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LENGTH: 238 amino acid
TYPE: amino acid
                                         TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-792-553-2
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COMPUTER READABLE FORM:
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FRAGMENT TYPE:
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Patent No. 6140132;
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Llopis, Juan
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/067001
CURRENT APPLICATION NUMBER: US/09/094,359
CURRENT FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 4.0
  Length 238;
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                                                 Indels
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                                                 5:
Score 1238; DB 3;
Pred. No. 6.8e-127;
1; Mismatches 5;
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Pred. No. 6.8e-127;
1; Mismatches 5;
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Patent No. 6150176
GENERAL INFORMATION:
APPLICANT: Taien, Roger Y.
APPLICANT: Miyawaki, Atsushi
APPLICANT: Llopis, Juan
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VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 1238; DB 3; Length 238;
Pred. No. 6.8e-127;
1; Mismatches 5; Indels
                 APPLICANT: Remington, S. James
TITLE OF INVENTION: FLUCRESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071031
CURRENT APPLICATION NUMBER: US/09/172,063
BARLIER APPLICATION UNMER: 09/094,359
BARLIER PILING DATE: 1998-10-13
BARLIER FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tsien, Roger Y.
APPLICANT: Tsien, Andrew B.
TITLE OF INVENTION: Assays for Protein Kinases Using
TITLE OF INVENTION: Pluorescent Protein Substrates
CORRESPONDENCE: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Storella, John S.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 02307Z-069000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 238
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ilarity 97.5%;
Conservative 1
APPLICANT: Wachter, Rebekka M.
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Aequorea victoria
US-09-172-063-2
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
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APPLICANT: Telen, Roger
TITLE OF INVENTIONS FULDESCENT PROTEIN SENSORS FOR DETECTION OF ANALYTES
TITLE OF INVENTIONS FULDORSCENT PROTEIN SENSORS FOR DETECTION OF ANALYTES
FILE REFERENCE: 0725/7/03201
CURRENT APPLICATION NUMBER: US/08/727,452A
CURRENT PILING DATE: 1996-03-20
EARLIER APPLICATION NUMBER: US/07/337,915
EARLIER FILING DATE: 1994-11-13
EARLIER FILING DATE: 1994-11-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTESC for Windows Version 3.0
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97.9%; Score 1238; DB 4; Length 238;
Best Local Similarity 97.5%; Pred. No. 6.8e-127;
Matches 232; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                               Score 1238; DB 3;
Pred. No. 6.8e-127;
1; Mismatches 5;
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Patent No. 6319669
                                                                                                                                                                                               97.9%;
TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 238 antino acids.
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US-08-727-452-2
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Best Local Similarity 97.5
Matches 232; Conservative
                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                      amino acid
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Best Local Similarity
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US-08-727-452-2
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Sequence 74, Application US/09129192C
Patent No. 649564
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Autora Biosciences Corporation
APPLICANT: Cubit, Andrew B.
TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications
TITLE APPLICATION NUMBER: US/09/129,192C
CURRENT APPLICATION NUMBER: US/09/129,192C
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.0
                                                                                                                            61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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; ORGANISM: Aequorea green fluorescent protein phosphorylation mutant
US-09-129-192C-74
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    Indels
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APPLICANT: Miyawaki, Atsushi
APPLICANT: Llopis, Juan
APPLICANT: Llopis, Juan
APPLICANT: Wachter, Rebeka M.
APPLICANT: Remington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICA
FILE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/09/602,641
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97.5%; Pred. No. 6.8e-127;
tive 1; Mismatches 5;
  1; Mismatches
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Conservative
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US-09-129-192C-74
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APPLICANT: Auora Biosciences Corporation
APPLICANT: Cubitt, Andrew B.
TILE OF INVENTION: Fluorescent B.
FILE REPERENCE: AUROL270 (08366/031001)
FILE REPERENCE: AUROL270 (08366/031001)
CURRENT APPLICATION NUMBER: US/09/129,192C
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.0
LENGTH: 238
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                                                                                         GENERAL INFORMATION:
APPLICANT: Fasher, Hugh
TITLE OF INVENTION: Rapidly Greening, Low Oxygen Mutant of
TITLE OF INVENTION: the Aequorea victoria Green Fluorescent Protein
FILE REPRENEUR: Rule 99-0011
CURRENT APPLICATION NUMBER: US/09/418,785
CURRENT PILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-16
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 238
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                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Aequorea victoria
PUBLICATION INFORMATION:
AUTHORS: Prasher, D.C. et al.
TITLE: Primary structure of the Aequorea victorea green-f
VOLUME: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
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97.5%; Pred. No. 6.8e-127;
tive 1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAGES: 229-233
DATE: 1992-01-01
DATABASE ACCESSION NUMBER: Genbank M62653
DATABASE ENTRY DATE: 1993-04-26
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                                                   ; Sequence 1, Application US/09418785 ; Patent No. 6414119
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97.5<del>8</del>;
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Best Local Similarity
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; ORGANISM: Aequorea
US-09-129-192C-2
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       RESULT 10
US-09-418-785-1
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APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Lippis, Juan
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEAGURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/057001
CURRENT APPLICATION NUMBER: US/09/704,463
CURRENT FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 09/094,359
PRIOR FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1238; DB 4; Length 238;
Pred. No. 6.8e-127;
1; Mismatches 5; Indels (
                                                                                                                                                                                                                                                            Length 238;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                  Query Match
97.9%; Score 1238; DB 4;
Best Local Similarity 97.5%; Pred. No. 6.8e-127;
Matches 232; Conservative 1; Mismatches 5;
                                                                  NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 238
CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/172,063
PRIOR FILING DATE: 1998-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09704463
Patent No. 6627449
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; ORGANISM: Aequorea victoria
US-09-602-641-2
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US-09-704-463-2
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Best Local Similarity 97.5
Matches 232; Conservative
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US-09-704-463-2
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181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
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                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Zolotukhin, Sergei
APPLICANT: Hauswirth, William W.
APPLICANT: Muzyczka, Nicholas
AITLE OF INVENTION: Humanized Green Fluorescent Protein
TITLE OF INVENTION: Genes and Methods
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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STATE: TX
COMPRES: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: ParentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/893,327
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97.5%; Pred. No. 9.3e-127;
tive 1; Mismatches 5;
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REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UFLA.062\KIT
TELECOMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: April 19, 2004, 15:08:34 Job time : 23 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/588,201
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                     Sequence 20, Application US/08893327
Patent No. 6020192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (512) 418-300
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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Matches 232; Conservative
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MOLECULE TYPE: protein
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CLASSIFICATION: 514
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US-08-893-327-20
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April 19, 2004, 14:55:50 ; Search time 60 Seconds (without alignments) 1120.772 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                           1586107 seqs, 282547505 residues
                                                                              - protein search, using sw model
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                                                                                                                                                                                                                                                                                BLOSUM62
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Perfect score:
                                                                                                                                                                                                                                                                              Scoring table:
                                                                            OM protein
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:* A Geneseq 29Jan04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* Post-processing: Minimum Match 0% .. Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Aawosana Green flu	Tellich		1879 GFP	9 Tell		13 Green	5310 Green	05 Jellyf			9	_						Aaw24232 Aemiorea		A	A	۵	3	
	ID		ABG76006	AAW31878	AAW31879	ABG76009	AAB73554	ADA25213	AAW05310	ABG76005	AAE34991	AAW31880	AAW31876	AAB73553	AAE34992	AAW05311	AAE34998	AAW05304	AAW05308	AAW24232	AAW76105	AAW40479	AAW65081	AAW76371	AAB73552	AAE16055
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VO DO IO	Abg76012 Jellyfish Abg75980 Jellyfish Aae34999 Aequorea				Adelboy Adducted Abg76613 Jellyfish Ade34990 Aequored Adw96330 Humanised
AAB16056 AAB16038 ABG32365	ABG76012 ABG75980 AAE34999 AAE34993	ABR44423 ADA25219 ADA25194	AAW22100 AAW2500	AAW65082 AAY43248 AAB73555	ABC16037 ABC346013 AAW96330
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ALIGNMENTS

RESULT 1

Green fluorescent protein mutant Y66W/N146I/M153T/V163A/N212K. AAW05309 standard; protein; 238 AA. (first entry) 02-APR-1997 AAW05309; AAW05309

Green fluorescent protein; GFP; jellyfish; Aequorea victoria; sea pansy; Renilla reniformis; differential gene expression; protein localisation; gene expression tracking; fluorescence.

Location/Qualifiers 212 /note= "N212K" /note= "N146I" 'note= "V163A" /note= "Y66W" /note= Misc-difference 146 Misc-difference Misc-difference Misc-difference Misc-difference WO9623810-A1 Synthetic.

94US-00337915 95WO-US014692 (REGC) UNIV CALIFORNIA. 13-NOV-1995; 10-NOV-1994; 88-AIG-1996

WPI; 1996-371370/37 Tsien RY, Heim R;

New modified Aequorea green fluorescent polypeptide(s) - having amino acid changes to provide prods. which exhibit different excitation and emission spectra.

Claim 11; Page ?; 39pp; English.

us-10-057-505-2-copy.rag

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protein (GFP) of the invention (see AAW0504 for the wild type protein).

The fluorescence of this protein is generated by cyclisation and coxidation of the Ser-Tyr-41's sequence at positions 65-67. Asquores GFP has two absorbance peaks, as opposed to the one absorbance peak seen in the related GFP from the sea pansy (Renilla reniformis). The modifications present in these sequences were created by subjecting the CDNA encoding this sequence to site directed mutagenesis using mutagenic CPR primers, or hydroxylamine treatment. These GFPs of the invention are modified to lead to the formation of products with markedly different CC excitetion and emission spectra. Vishly distinct colours, and increased intensities of emission make these products useful in a wide variety of contexts, such as tracking of differential gene expression and protein localisation. The mutations can also be created to modify the encoded GFP KK
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Pred. No. 1.7e-122;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                 Sequence 238 AA;
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note= "Wild-type Asn substituted by Ile"
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                                                                                                                   Location/Qualifiers
                                                                                                                                                 Misc-difference 153
                                                                                                                                                              Misc-difference 163
                                                                                                                                    Misc-difference
                                                                                                                                                                          Misc-difference
                                                                                                                        Misc-difference
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07-NOV-2002.

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comprising a donor or acceptor funcescent protein moiety (e.g. jellyfish green fluorescent protein, GPP) or a linker moiety that couples the donor and acceptor moieties. Also include are a recombinant nucleic acid coding for the tandem fluorescent protein construct, an expression of the tandem fluorescent protein construct, an expression control sequences operatively linked to a sequence coding for the expression of the tandem fluorescent protein construct, a host cell transfected with the expression vector. Getermining whether a sample contains an enzyme or whether a compound a lers the activity of an enzyme, determining the amount of activity of an enzyme, determining the amount of activity of an enzyme, determining the amount of activity of an enzyme in a cell and testing for cleavage enzyme activity. The tandem fluorescent protein construct is useful in enzymatic assays, using the donor and acceptor moieties. The tandem fluorescent proteins are particularly useful in assays for protease activity. Proteases play an essential role in many disease processes e.g. Alzheimer's disease, hypertension, inflammation, apoptosis and AIDS (acquired immunodeficiency syndrome). Tandem fluorescent proteins were constructed comprising mutants of GFP with altered fluorescent spectra. The present sequence of syndrome). Tandem fluorescent proteins were constructed comprising mutants of GFP with altered fluorescent spectra. The present sequence constructed comprising information in the specification but was created by the indexer using the information in the specification and the wild-type GFP protein appearing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VIITESWGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKIRAEVKFEGDTLV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New tandem fluorescent protein construct comprising a donor or acceptor fluorescent protein moiety or a linker moiety that couples the donor and acceptor moieties, useful in enzymatic assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK
                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to a tandem fluorescent protein construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ā
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                                                                                                                                                                           Cubitt A;
                                            96US-00594575.
  2002US-00057505.
                                                                 97US-00792553.
                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page; 34pp; English.
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                                                                                                                                 (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                             Heim R,
                                                                                                                                                                                                                     WPI; 2003-247255/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 236; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 238 AA;
25-JAN-2002;
                                            31-JAN-1996;
                                                               31-JAN-1997;
13-SEP-1999;
                                                                                                                                                                           Tsien RY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW31878;
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AAW31878
ID AAW3
XX
AC AAW3
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DT 03-F
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example, the linker moiety contains many recognition sites for proteases, including trypsin, calpain and enterokinase. The donor and acceptor moieties exhibit fluorescent resonance energy transfer (FRET) when they are cleaved. The constructs are used in enzymatic assays and can be used to isolate new enzymes or enzyme inhibitors or promoters. The specific activity of enzyme (in vivo and in vitro) and compounds altering enzyme activity can be obtained. FRET and hence activity of specific compounds is measured from the acceptor or donor moiety or maybe obtained using a riatio between the two. Note: The present sequence does not appear in the specification; it has been made by modifying the native GFP sequence, and adding the linker moiety in the appropriate place

888888888888888888

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Gaps

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1; Indels Length

99.4%; Score 1257; DB 2; 98.7%; Pred. No. 8e-122; ive 2; Mismatches 1;

Best Local Similarity 98.7 Matches 235, Conservative

Query Match Best Local 8

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Sequence 501 AA;

9

264 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLILKFICTTGKLPVPWPTL 323 VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120 324 VITFSWGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 383 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180

61

121

181

1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL

HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238

444 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHWYLLEFVTAAGITHGMDELYK

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This protein sequence is that of a novel tandem fluorescent protein construct, made using Aequorea victoria (North West Pacific jellyfish) green fluorescent protein (GFP) variants S65c and W7. W7 fluoresces at a shorter wavelength than GFP. The construct comprises a donor (e.g. S65c) and an acceptor (e.g. W7) fluorescent protein moiety (donors and coceptors can be green or blue fluorescent proteins), and a linker coupling them. Preferably, the donor is positioned at the N-terminus of the polypeptide relative to the acceptor. The linker moiety is a peptide 5-50 amino acids in length containing a protease cleavage site. In this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tandem fluorescent protein constructs - have donor and acceptor moieties exhibiting fluorescent linked via cleavable peptide linker, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AURO-) AURORA BIOSCIENCES CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-402615/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzymatic assays.
                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9728261-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isien RY,
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Val substituted with Ala"

/label= V163A /note= "wild type 'note= "wild type

label=

Met substituted with Thr"

/label= N212K /note= "wild type Asn substituted with Lys"

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North West Pacific jellyfish; green fluorescent protein; GFP; S6SC; fluorescent resonance energy transfer; FRET; enzymatic assay; W7; enzyme inhibitor; enzyme promoter; FCR primer; protease cleavage site; Tandem fluorescent protein construct; blue fluorescent protein.
GFP variants S65C and W7 tandem fluorescent protein construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "wild type Tyr substituted with Trp'
                                                                                                                                                                                                                                                                                                                                        /note= "wild type Ser substituted with Cys" 239. .264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "wild type Asn substituted with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            758. .259 - "
|label= trypsin_enterokinase_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                       250. .251
/label= trypsin_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              calpain_cleavage_site
                                                                                                                                                                                                                                                                      /label= S65C_GFP_variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265. .501 -- -- // Jabel= W7_GFP_variant
                                                                                                                                                                                                                                                                                                                                                                                  label= linker_moeity
                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label= N146L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= Y66W
                                                                                                                                                                                                                                                                                                                     /label= S65C
                                                                                                                                                                                                                                                                                                                                                                                                                                                    253. .254
/label= ca
                                                                                                                                                                                                                                                    .238
                                                                                                                                                                             Aequorea victoria.
                                                                                                                                                                                                                                                                                           Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cleavage-site
                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                    Protein
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fluorescent resonance energy transfer; FRET; enzymatic assay; W7; enzyme inhibitor; enzyme promoter; PCR primer; protease cleavage site; Tandem fluorescent protein construct; blue fluorescent protein. North West Pacific jellyfish; green fluorescent protein; GFP; 865C; GFP variants S65T and W7 tandem fluorescent protein construct. /label= S65C /note= "wild type Ser substituted with Thr" 239. .264 /label= linker_moeity /note= "wild type Tyr substituted with Trp" Misc-difference 409 . 259 | Tabel = trypsin_enterokinase_cleavage_site 250. .251 /label= trypsin_cleavage_site 253. 254 /label= calpain_cleavage_site 1. .238
/label= S65T_GFP_variant 265. .501 /label= W7_GFP_variant Location/Qualifiers Ą. AAW31879 standard; protein; 501 /label= Y66W (first entry) Misc-difference 329 Aequorea victoria. Misc-difference Cleavage-site Cleavage-site 03-FEB-1998 Synthetic Peptide Protein AAW31879

Cubitt A;

Heim R,

97WO-US001457 96US-00594575.

Tue Apr

Tabel= M153T 'note= "wild type Met substituted with Thr"

'note= "wild type Asn substituted with Leu'

label= N146L

"wild type Asn substituted with Lys"

Val substituted with Ala"

/label= V163A /note= "wild type

/label= N212K

/note=

97WO-US001457.

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Tandem fluorescent protein constructs - have donor and acceptor moieties exhibiting fluorescent linked via cleavable peptide linker, useful in
                                                                                                           (REGC ) UNIV CALIFORNIA. (AURO-) AURORA BIOSCIENCES CORP.
                                                                                                                                                                        Claim 3; Page; 88pp; English.
                                                                                                  96US-00594575
                                                                                                                                         WPI; 1997-402615/37
                                                                                                                              Heim R,
                                                                                                                                                              enzymatic assays.
            Misc-difference
                            Misc-difference
                                            Misc-difference
                                                                 WOS728261-A1
                                                                                       31-JAN-1997;
                                                                                                  31-JAN-1996;
                                                                            07-AUG-1997
                                                                                                                             Tsien RY,
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Cubitt A;

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This protein sequence is that of a novel tandem fluorescent protein construct, made using Aequorea victoria (North West Pacific jellyfish) or green fluorescent protein (GFP) variants S6F and W7. W7 fluoresces at a shorter wavelength than GFP. The construct comprises a donor (e.g. S65T) and an acceptor (e.g. W7) fluorescent protein molety donors and acceptors can be green or blue fluorescent proteins), and a linker coupling them. Preferably, the donor is positioned at the N-terminus of the polypeptide relative to the acceptor. The linker molety is a peptide 5-50 amino acids in length containing a protease cleavage site. In this example, the linker molety contains many recognition sites for proteases, including trypsin, calpain and enterokinase. The donor and acceptor moleties exhibit fluorescent resonance energy transfer (FRET) when they are cleaved. The constructs are used in enzymatic assays and can be used to isolate new narymes or enzyme inhibitors or promoters. The specific compounds cativity of enzyme (in vivo and in vitro) and compounds altering enzyme acceptor or donor molety or maybe obtained using a ratio between the two. Note: The present sequence does not appear in the specification; it has been made by modifying the native GFP sequence, and
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                                                                                                                             VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                      323
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                                                                                                                                                                                                                                       443
                                                                       9
                                                                                                                                                                                                                                                             181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                        264 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLDVPWPTL
                                                                                                                                                                                                                             NRIELKGIDFKEDGNILGHKLEYNYLSHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD
                                                                MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                       Gaps
                                       ·,
 99.4%; Score 1257; DB 2; Length 501; 98.7%; Pred. No. 8e-122; Live 2; Mismatches 1; Indels (
                                  Conservative
               Similarity
Query Match
Best Local Simi
Matches 235;
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compitaing adonor or acceptor fluorescent protein moiety (e.g. jellyfish green fluorescent protein moiety that couples the donor and acceptor moiety expectations of the tandem fluorescent protein construct, an expression of the tandem fluorescent protein construct, an expression vector comprising expression control sequences operatively linked to a sequence coding for the expression of the tandem fluorescent protein construct, a host cell transfected with the expression vector construct, a host cell transfected with the expression vector, a lost cell transfected with the expression vector, at letters the activity of an enzyme or whether a compound an enzyme in a cell and testing for cleavage enzyme activity of an enzyme fluorescent protein construct is useful in enzymeactivity. The tandem fluorescent protein construct is useful in enzymeactivity, using the principle of fluorescent resonance energy transfer (FRET) between the

The invention relates to a tandem fluorescent protein construct

Claim 18; Page; 34pp; English

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New tandem fluorescent protein construct comprising a donor or acceptor fluorescent protein moiety or a linker moiety that couples the donor and acceptor moieties, useful in enzymatic assays.
Vellyfish; enzyme; green fluorescent protein; GFP; FRET; mutant;
fluorescent resonance energy transfer; tandem fluorescent protein;
enzymatic assay; Alzheiner's disease; hypertension; inflammation;
apoptosis; AIDS; acquired immunodeficiency syndrome; mutein.
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                                                                                                                                                                                                                                                                                   Trp"
                                                                                                                                                                                                                                                                                                      Ile"
                                                                                                                                                                                                                                           'note= "Wild-type Phe substituted by
                                                                                                                                                                                                                                                               substituted by
                                                                                                                                                                                                                                                                                                                       'note= "Wild-type Met substituted by
                                                                                                                                                                                                                                                                                                                                             substituted by
                                                                                                                                                                                                                                                                                                                                                              /note= "Wild-type Asn substituted by
                                                                                                                                                                                                                                                                                                   note= "Wild-type Asn substituted
                                                                                                                                                                                                                                                                                  substituted
                                                                                                                                                                                                                                                             'note= "Wild-type Ser
                                                                                                                                                                                                                                                                                'note= "Wild-type Tyr
                                                                                                                                                                                                                                                                                                                                            'note= "Wild-type Val
                                                                                                                                                                                                                         Location/Qualifiers
                                                           ABG76009 standard; protein; 238 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-00792553.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heim R, Cubitt
                                                                                                 (first entry)
                                                                                                                      Jellyfish GFP mutant W1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-247255/24.
                                                                                                                                                                                                                                                                                                             Misc-difference 153
                                                                                                                                                                                                                                                    Misc-difference 65
                                                                                                                                                                                         Aequorea victoria.
Synthetic.
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                                                                                                                                                                                                                                                                                           Misc-difference
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13-SEP-1999;
                                                                                                  30-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsien RY,
                                                                              ABG76009;
                                        RESULT 5
                                                    ABG7600
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us-10-057-505-2-copy.rag

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Page

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donor and acceptor moieties. The tandem fluorescent proteins are particularly useful in assays for protease activity. Proteases play an essential role in many disease processes e.g. Alzheimer's disease, hypertension, inflammation, apoptosis and AIDS (acquired immunodeficiency syndrome). Tandem fluorescent proteins were constructed comprising mutants of GFP with altered fluorescent spectra. The present sequence represents a mutant GFP suitable for incorporation into a tandem fluorescent protein of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the information in the specification and the wild-type GFP protein appearing
                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VITLIWGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                   VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                             Length 238;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                         Score 1250; DB 6;
Pred. No. 1.4e-121;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                       98.8%;
98.3%;
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                   Sequence 238 AA;
                                                                                                                                                                                                                                                                                     Matches 234;
                                                                                                                                                                                                                                                                                                                                                                                                   19
                                                                                                                                                                                                                                                       Query Match
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Phenotype selection; non-selectable; fusion protein; stable expression; selectable marker; antibiotic resistance gene; Bscherichia coli; green fluorescent protein; GFP; GFPRI; pGFP; mutant; mutein.
                                                       Green fluorescent protein mutant, GFPR1.
            AAB73554 standard; protein; 238
                                        (first entry
                                                                                                 Aequorea victoria
                                         07-AUG-2001
                           AAB73554;
RESULT
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/note= "Ala replaces wild-type Val" Location/Qualifiers Misc-difference 163 Synthetic.

WO200129225-A1

21-OCT-1999; 99US-0160461P. 22-FEB-2000; 2000US-00510097; 29-MAR-2000; 2000WO-US008477 21-OCT-1999; 26-APR-2001

(PANO-) PANORAMA RES INC

WPI; 2001-282162/29. Balint RF;

N-PSDB; AAH20247

Obtaining cells expressing mutant protein, comprises selecting from cells

30-OCT-2002

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The invention relates to methods whereby variants of proteins which do not confer selectable phenotypes can be selected for stable expression in confer selectable phenotypes can be selected for stable expression in confer selectable phenotypes can be selected for expression in the host cells, for obtaining a mutant protein with enhanced stability relative to the wild-type protein, and for identifying peptides that stabilise an unstable protein. The methods all involve expressing the protein of interest as a fusion with a protein that can confer a selectable phenotype, such as an antibiotic resistance protein. The transformed host cells are then grown under selective pressure (e.g., presence of antibiotic). The cells able to grow under such conditions are those which contain fusion proteins which are optimised for expression or which are contain fusion proteins which are optimised for expression or which are contain fusion proteins which are optimised for expression or which are contain to rate of synthesis of the selectable marker. The invention also discloses mutants of green fluorescent protein (GFPP) selected for sequence represents a GFP mutant (GFPRI) which has increased stability callid-type GFP. The present sequence is not shown in the specification, but was derived from the plasmid pGFP (GenBank accession number U17997) and the information given on page 23 of the specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 VITESYGVQCFSRXPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDILV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKONGIKANFKIRHNIEDGSVOLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
transformed with library of mutagenized protein coding sequences joined to selector protein, which confers growth under selective conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; GFP; jellyfish; marker protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.2%; Score 1242; DB 4;
97.9%; Pred. No. 9.8e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Green fluorescent protein mutant, V163A-GFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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                                                          Example 2; Page; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 97.9
Matches 233, Conservative
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Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Green fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 238 AA;
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Thomas N;

Michael NP,

UK LID

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(GFP) mutants containing an amino acid substitution at positions 64 and 175, and additionally an amino acid substitution at either proistion 65 or 222. The mutants of the invention are particularly F64L-5176-E22G-GFP (ADA25195) or F64L-S67T-S175G-GFP (ADA25196). GFP mutants of the invention exhibit enhanced fluorescence relative to wild type GFP when expressed in non-homologous cells at temperatures above 30 degrees Celsius, and excited at 490 nm. The mutants can also be detected in mammalian cells at lower levels of expression and with increased constituty relative to wild type GFP. The GFP mutants of the invention are useful as non-toxic markers for selection of transfected cells, as protein labels in living and fixed cells, as markers in cell or organalle fusion, for visualising translocation of intracellular proteins to a specific organelle, as secretion markers, as genetic reporters or protein and gene expression in transgenic animals, as cell or organelle integrity markers, as transfection markers as markers to be used in combination with fluorescent activated cell sorting (FACS), as cell-represent and proper activated cell sorting (FACS), as cell-represent and proper activated cell sorting for the confine probes working at near physiological concentrations, for the probes working at near physiological concentrations, for the confine probes working at near physiological concentrations, for the probes working at near physiological concentrations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 performing transposon vector mutagenesis, and as reporters for bacterial detection. The present sequence represents an Aequorea victoria GFP mutant used in an example of the invention. Note: The present sequence is not shown in the specification, but is derived from the wild-type GFP sequence shown in Fig 2 and the information given on page 24.
                                                                                                                                                                                                                                                                                                              Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to Aequorea victoria green fluorescent protein
                                                                                                     (AMSH ) AMERSHAM PHARMACIA BIOTECH (AMSH ) AMERSHAM BIOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page; 52pp; English.
                                                    23-APR-2001; 2001GB-00009858.
28-SEP-2001; 2001GB-00023288
                                                                                                                                                                                Stubbs SLJ, Jones AE,
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N-PSDB; ADA25193.
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Indels Score 1242; DB 6; Pred. No. 9.8e-121; 1; Mismatches 4; 1; 98.2%; Conservative 181 181 a ð

Sequence 238 AA;

61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120 61 VITESYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDILV 120 121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180 09 1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLEFVTAAGITHGMDELYK 238 1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL ·. Length 238;

AAW05310 standard; protein; 238 (first entry) 02-APR-1997 AAW05310; AAW05310 1D AAW0 XX AC AAW0 XX DT 02-A RESULT 8

Green fluorescent protein; GPP; jellyfish; Aequorea victoria; sea pansy; Renilla reniformis; differential gene expression; protein localisation; gene expression tracking; fluorescence. Green fluorescent protein mutant Y66H/Y145F. Location/Qualifiers /note= "Y145F" 'note= "Y66H" 95WO-US014692. 94US-00337915. (REGC) UNIV CALIFORNIA WPI; 1996-371370/37 Misc-difference 145 Misc-difference 66 rsien RY, Heim R; 13-NOV-1995; 10-NOV-1994; WO9623810-A1 38-AUG-1996 Synthetic

New modified Aequorea green fluorescent polypeptide(s) - having amino acid changes to provide prods. which exhibit different excitation and emission spectra.

Claim 10; Page ?; 39pp; English.

AAW05305-W05312 represent Aequorea victoria (jellyfish) green fluorescent protein (GFP) of the invention (see AAW05304 for the wild type protein). The fluorescence of this protein is generated by cyclisation and oxidation of the Ser-Tyr-GJy sequence at positions 65-67. Aequorea GFP has two absorbance peaks, as opposed to the one absorbance peak seen in the related GFP from the sea pairsy (Renilla reniformis). The modifications present in these sequences were created by subjecting the CDNA encoding this sequence to site directed mutagenesis using mutagenic CPK primars, or hydroxylamine treatment. These GFPs of the invention are modified to lead to the formation of products with markedly different excitation and emission spectra. Visibly distinct colours, and increased intensities of emission make these products useful in a wide variety of contexts, such as tracking of differential gene expression and protein localisation. The mutations can also be created to modify the encoded GFP so that it only possesses one absorbance peak

NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180 121 NRIELKGIDFKEDGNILGHKLEYNFNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVOLAD 180 9 9 181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238 61 VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL ; Length 238; Indels Score 1241; DB 2; Pred. No. 1.2e-120; 0; Mismatches 5; 98.18; Matches 233; Conservative Similarity Query Match Best Local S 121 g à g 셤 ð ð

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ABG76005 standard; protein; 238 AA.
             30-APR-2003 (first entry)
                 Jellyfish GFP mutant P4-3
                                                                 31-JAN-1996;
31-JAN-1997;
13-SEP-1999;
                                                        07-NOV-2002
                                   Synthetic
        ABG76005;
RESULT 9
ABG76005
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The invention relates to a tandem fluorescent protein construct comprising a donor or acceptor fluorescent protein molety (e.g. jellyfish green fluorescent protein, or a linker molety (e.g. jellyfish green fluorescent protein, or a complex the donor and acceptor moleties. Also include are a recombinant nucleic acid coding for expression of the tandem fluorescent protein construct, an expression control sequences operatively linked to a sequence coding for the expression of the tandem fluorescent protein construct, a host cell transfected with the expression vector, determining whether a sample contains an enzyme or whether a compound alters the activity of an enzyme, determining the amount of activity of an enzyme in a cell and testing for cleavage enzyme activity. The tandem fluorescent protein construct is useful in enzymatic assays, using the control of the construct is useful in enzymatic assays, using the fluorescent protein construct is useful in enzymatic assays, using the control of in many disease processes activity. Proteases play an essential role in many disease processes activity. Proteases play an essential role in many disease processes activity. Proteases play an essential role in many disease processes activity. Proteases play and hypertension, inflammation, apoptosis and AIDS (acquired immunodeficiency syndrome). Tandem fluorescent proteins were constructed comprising the fluorescents a mutant GPP suitable for incorporation into a fuel invention. Note: The present sequence is not shown in the specification but was created by the indexer using the information in the specification and the wild-type GFP protein appearing as a shorts and and an enter and the wild-type GFP protein and the wild-type GFP p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New tandem fluorescent protein construct comprising a donor or acceptor fluorescent protein moiety or a linker moiety that couples the donor and acceptor moieties, useful in enzymatic assays.
Jellyfish; enzyme; green fluorescent protein; GFP; FRET; mutant; fluorescent resonance energy transfer; tandem fluorescent protein; enzymatic assay; Alzheimer's disease; hypertension; inflammation; apoptosis; AlDS; acquired immunodeficiency syndrome; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild-type Tyr substituted by His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Wild-type Tyr substituted by Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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97US-00792553.
99US-00396003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-2002; 2002US-00057505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                                                                                       Aequorea victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
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Sequence 238 AA;

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                                                                                                                                                                                                     NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to chimeric phosphorylation indicators comprising a phosphorylation polypeptide and a fluorescent protein or in operative linkage, a donor molecule, a phosphorylatable domain, a phosphorylation becaule the phosphomainoacid binding domain (PAABD) and an acceptor molecule. The phosphomainoacid binding domain (PAABD) and an acceptor molecule. The phosphorylation indicators of the invention are useful for detecting kinases or phosphatases in a biological sample. They are also useful in high throughput analysis e.g. for detecting a kinase inhibitor or phosphatase inhibitor. The present sequence is Aequorea victoria mutant green fluorescent protein (GFP; NH461) used in the invention. Note: This sequence is not shown in the specification but is derived from Aequorea victoria wild-type GFP shown as SEQ ID NO: 2 in column 53-54 of the
                                                                                                                                                                                                                                                                       181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                              Phosphorylation indicator, fluorescent protein, detection, phosphatase, kinase, green fluorescent protein, GFP, mutant, mutein.
                                                                                                                                                                                                                            1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                      61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel chimeric phosphorylation indicators, useful for detecting kinase/phosphatase in samples, has donor molecule, phosphorylatable domain, phosphoaminoacid binding domain, and acceptor molecule, in operative linkage.
                                      0
       Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Wild-type Asn substituted with Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aequorea victoria mutant green fluorescent protein (N1461).
                                                                   1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICT
                                      Indels
   Score 1241; DB 6;
Pred. No. 1.2e-120;
0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                         AAE34991 standard; protein; 238 AA
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 98.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                     Conservative
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Query Match
Best Local Similarity
Matches 233; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                             AAE34991;
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07-AUG-1997.
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                                                                                                  VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                             61 VITESYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDILV 120
                                                                                                                                             121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                    9
                                                                                   9
                                                                                                                                                                     HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHWVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                              North West Pacific jellyfish; green fluorescent protein, GFP; P4-3; fluorescent resonance energy transfer; FRET; enzymatic assay; W7; enzyme inhibitor; enzyme promoter; PCR primer; protease cleavage site; Tandem fluorescent protein construct; blue fluorescent protein.
                                                                              1 MSKGEELFTGVVPILVELDGDVNGHKRSVSGEGEGDATYGKLTLKFICTTGKLDVPWPTL
                                                                 1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                    Gaps
                                                  ·;
                                                                                                                                                                                                                                                                                 GFP variants P4-3 and W7 tandem fluorescent protein construct.
                                   Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                      /label= Y66H
/note= "wild type Tyr substituted with His"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        "wild type Tyr substituted with Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "wild type Asn substituted with Leu"
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| Jabel = trypsin_enterokinase_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "wild type Tyr substituted with Trp'
                                                  Indels
                                 Score 1241; DB 6;
Pred. No. 1.2e-120;
2; Mismatches 4;
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/label= trypsin_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253. .254
/label= calpain_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                      /label= P4-3_GFP_variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65. 501 -
label= W7_GFP_variant
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/label= linker_moeity
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                              98.1%;
milarity 97.5%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 426
/label= V163A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= N146L
                                                                                                                                                                                                                                                                                                                                                                                                                                'label= Y145F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= M153T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= Y66W
                                                                                                                                                                                                                                                                (first entry)
specification (AAE34957)
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
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                                        Similarity
                                                                                                                                                                                                                                                                                                                                                    Aequorea victoria
                Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
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                                                                                                                                                                                                                                                                 03-FEB-1998
                                               Matches 232;
                                                                                                                                                                                      181
                                                                                                   . 19
                               Query Match
                                                                                                                                                                                                                                                AAW31880;
                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
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This protein sequence is that of a novel tandem fluorescent protein construct, made using Aequorea victoria (North West Pacific jellyfish) green fluorescent protein (GPP) variants P4-3 and W7. Both of these donor (e.g. P4-3) and an acceptor (e.g. W7) fluorescent protein moiety (donors and acceptors can be green or blue fluorescent protein moiety (inher coupling them. Preferably, the donor is positioned at the N-terminus of the polypeptide relative to the acceptor. The linker moiety is a peptide 5-50 amino acids in length containing a protease cleavage of the proteases, including trypsin, calpain and enterokinase. The donor and acceptor moieties exhibit fluorescent resonance energy transfer (FRET) when they are cleaved. The constructs are used in enzymatic assays and can be used to isolate new enzymes or enzyme inhibitors or promoters. The specific activity of enzyme (in vivo and in vitro) and compounds altering enzyme activity can be obtained. FRET and hence activity of specific and a commentation and entering and accepting activity can be obtained. FRET and hence activity of specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          compounds is measured from the acceptor or donor moiety or maybe obtained using a ratio between the two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VITFSHGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tandem fluorescent protein constructs - have donor and acceptor moieties exhibiting fluorescent linked via cleavable peptide linker, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSKGEELFIGVVPILVELDGDVNGHKPSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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                                                                       /label= N212K
/note= "wild type Asn substituted with Lys"
/note= "wild type Val substituted with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW31876 standard; protein; 514 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA.
(AURO-) AURORA BIOSCIENCES CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsien RY, Heim R, Cubitt A;
                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-00594575.
                                                                                                                                                                                                                                                                                                                                                        97WO-US001457.
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Best Local Similarity 97.9°
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-402615/37
                                          Misc-difference 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enzymatic assays.
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                                                                                                                                                                                                                                                                                                                                                        31-JAN-1997;
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Gaps

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Length 514; Indels 9

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WPI; 1997-402615/37
                                                                                                                                           'sien RY, Heim R,
                               Aequorea victoria.
                                                                                                                                                            enzymatic assays.
                                                  Misc-difference
                                                                                       Misc-difference
                                                                                                Misc-difference
                                                                Cleavage-site
                                                                      Cleavage-site
                                                                            Cleavage-site
                                                                                                           WO9728261-A1
                                                                                                                       31-JAN-1997;
                                                                                                                             31-JAN-1996;
                                                                                                                 07-AUG-1997
                            Synthetic.
                                       Peptide
                                             Protein
                                                           Peptide
                                                                                  Protein
                                                                                                                                     (AURO-)
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activity of enzyme (in vivo and in vitro) and compounds altering enzyme activity can be obtained. FRET and hence activity of specific compounds is measured from the acceptor or donor moiety or maybe obtained using a ratio between the two. Note: The present sequence does not appear in the specification; it has been made by modifying the native GFP sequence, and adding the linker moiety in the appropriate place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                         277 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 336
                                                                                                                                                                                                                                                                                                                                                                                                         VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                      337 VITFSHGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 NRIELKGIDFKEDGNILGHKLEYNFNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Obtaining cells expressing mutant protein, comprises selecting from cells transformed with library of mutagenized protein coding sequences joined to selector protein, which confers growth under selective conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to methods whereby variants of proteins which do not confer selectable phenotypes can be selected for stable expression in host cells (especially Escherichia coli). The methods can be used to obtain mutants of a desired protein optimised for expression in the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phenotype selection; non-selectable; fusion protein; stable expression; selectable marker; antibiotic resistance gene; Escherichia coli; green fluorescent protein; GFP; GFPuv; pGFPuv; mutant; mutein.
                                                                                                                                                                                                                                                                                                            1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                  Score 1241; DB 2;
Pred. No. 3.8e-120;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Green fluorescent protein variant GFPuv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB73553 standard; protein; 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-FEB-2000; 2000US-00510097.
                                                                                                                                                                                                                    98.1%;
97.9%;
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Best Local Similarity 97.9
Matches 233; Conservative
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                                                                                                                                                                     Sequence 514 AA;
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construct, made using Aequorea victoria (North West Pacific jellyfish)

green fluorescent protein (GFP) variants SS5C and P4-3. P4-3 fluoresces

at a shorter wavelength than GFP. The construct comprises a donor (e.g.

SS5C) and an acceptor (e.g. P4-3) fluorescent protein moiety (donors and

acceptors can be green or blue fluorescent proteins), and a linker

coupling them. Preferably, the donor is positioned at the N-terminus of

the polypeptide relative to the acceptor. The linker moiety is a peptide

5-50 amino acids in length containing a protease cleavage site. In this

example, the linker moiety contains many recognition sites for proteases,

including trypsin, calpain and enteroxinase. The donor and acceptor

moieties exhibit fluorescent resonance energy transfer (FRET) when they

are cleaved. The constructs are used in enzymatic asseys and can be used

to isolate new enzymes or enzyme inhibitors or promoters. The specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tandem fluorescent protein constructs - have donor and acceptor moieties exhibiting fluorescent linked via cleavable peptide linker, useful in
                                                                                                    North West Pacific jellyfish; green fluorescent protein; GFP; S6SC; fluorescent resonance energy transfer; FRET; enzymatic assay; P4-3; enzyme inhibitor; enzyme promoter; PCR primer; protease cleavage site; Tandem fluorescent protein construct; blue fluorescent protein.
                                                    GFP variants S65C and P4~3 tandem fluorescent protein construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with His"
                                                                                                                                                                                                                                                                                                                                                                                                                                            label= 865C
'note≈ "wild type Ser substituted with Cys"
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/label= trypsin_enterokinase_cleavage_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note≈ "wild type Tyr substituted
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.266
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                                                                                                                                                                                                                                                                                                                           1. .10
| label= polyhistidine_tag
                                                                                                                                                                                                                                                                                                                                                                      77. .514 - Tabel= P4-3_GFP_variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252. .276
/label= linker_moiety
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Y145F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-US001457
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/label= tr
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          03-FEB-1998 (first entry)
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cells, for obtaining a mutant protein with enhanced stability relative to the wild-type protein, and for identifying peptides that stabilise an unstable protein. The methods all involve expressing the protein of interest as a fusion with a protein that can confer a selectable of phenotype, such as an antibiotic resistance protein. The transformed host cells are then grown under selective pressure (e.g., presence of antibiotic). The cells able to grow under such conditions are those which contain proteins which are optimised for expression or which are more stable, as this property will also correlate with an increased amount or rate of synthesis of the selectable marker. The invention also discloses mutants of green fluorescent protein (GFP) selected for increased stability using the method of the invention. The present sequence represents a GFP variant (GFPuv) as encoded by plasmid pGFPuv (Gensbank UG2636), which was used in an exemplification of the invention. The present sequence is not shown in the specification, but was derived for thom GenBank accession number UG2636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VITESYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIISFKDDGNYKTRAEVKFEGDTLV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VITESXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphorylation indicator; fluorescent protein; detection; phosphatase;
                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                  Score 1240; DB 4; Length 238; Pred. No. 1.6e-120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aequorea victoria mutant green fluorescent protein (M153T).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild-type Met substituted with Thr"
                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kinase; green fluorescent protein; GFP; mutant; mutein
                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE34992 standard; protein; 238
                                                                                                                                                                                                                                                                                                                                 98.0%;
97.9%;
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                                                                                                                                                                                                                                                                                                                                                   Local Similarity 97.9
nes 233; Conservative
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                                                                                                                                                                                                                                                                                                Sequence 238 AA;
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WPI; 2003-148474/14

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 NRIELKGIDFKEDGNILGHKLEYNYNSHNYYITADKQKNGIKVNFKIRHNIEDGSVQLAD 180
                                                                                                                                       The present invention relates to chimeric phosphorylation indicators comprising a phosphorylation polypeptide and a fluorescent protein or in operative linkage, a donor molecule, a phosphorylatable domain, a phosphorylation demain (PAABD) and an acceptor molecule. The phosphoaminoacid binding domain (PAABD) and an acceptor molecule. The phosphorylation indicators of the invention are useful for detecting kinases or phosphatases in a biological sample. They are also useful in high throughput analysis e.g. for detecting a kinase inhibitor or phosphatase inhibitor. The present sequence is Aequorea victoria mutant green fluorescent protein (GFP; MIS3T) used in the invention. Note: This sequence is not shown in the specification but is derived from Aequorea victoria wild-type GFP shown as SEQ ID NO: 2 in column 53-54 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Green fluorescent protein; GFP; jellyfish; Aequorea victoria; sea pansy
Renilla reniformis; differential gene expression; protein localisation;
gene expression tracking; fluorescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
             Novel chimeric phosphorylation indicators, useful for detecting kinase/phosphatase in samples, has donor molecule, phosphorylatable domain, phosphoaminoacid binding domain, and acceptor molecule, in operative linkage.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1240; DB 6;
Pred. No. 1.6e-120;
2; Mismatches 4;
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163
/note= "V163A"
                                                                                                         Disclosure; Col; 38pp; English.
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Best Local Similarity 97.5%;
Matches 232; Conservative
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AAW05305-W05312 represent Aequorea victoria (jellyfish) green fluorescent protein (GFP) of the invention (see AAW05304 for the wild type protein. The fluorescence of this protein is generated by cyclisation and coxidation of the Ser-Tyr-Gly sequence at positions 65-67. Aequorea GFP has two absorbance peaks, as opposed to the one absorbance peak seen in the two absorbance peak seen in the testated GFP from the see pansy (Renilla reniformis). The related GFP from the see pansy (Renilla reniformis). The modifications present in these sequences were created by subjecting the CDNA encoding this sequence to site directed mutagenesis using mutagenic CDNA encoding this sequence to site directed mutagenesis using mutagenic councillated to lead to the formation of products with markedly different excitation and emission make these products useful in a wide variety of intensities of emission make these products useful in a wide variety of contexts, such as tracking of differential gene expression and protein localisation. The mutations can also be created to modify the encoded GFP contact in tonly possesses one absorbance peak
                                                                                                                                                                                                                                                                                                                                                               New modified Aequorea green fluorescent polypeptide(s) - having amino acid changes to provide prods. which exhibit different excitation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
97.9%; Score 1239; DB 2; Length 238;
Best Local Similarity 97.9%; Pred. No. 2e-120;
Matches 233; Conservative 1; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Page ?; 39pp; English.
Misc-difference 212
/note= "N212K"
                                                                                                                                                      95WO-US014692
                                                                                                                                                                                              94US-00337915
                                                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                       WPI; 1996-371370/37
                                                                                                                                                                                                                                                                           Psien RY, Heim R;
                                                                                                                                                                                                                                                                                                                                                                                                           emission spectra.
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61 VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120 61 VITESWGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKOKNGIKANFKIRHNIEDGSVOLAD 180 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238 181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLBFVTAAGITHGMDELYK 238 1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 0; Gaps 121 181 qq qq à à

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9

Search completed: April 19, 2004, 15:05:58 Job time : 61 secs

18.

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

using sw model OM protein - protein search,

April 19, 2004, 14:56:35 ; Search time 17 Seconds (without alignments) 728.982 Million cell updates/sec

Run on:

Perfect score:

US-10-057-505-2-COPY 1265 1 MSKGEELFTGVVPILVELDG......VLLEFVTAAGITHGMDELYK 238 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	in administration of COAC	2 campylobs		P21951 saccharomyc		wiggl	_					rhizo	P49610 streptococc		P00467 clostridium			discopy		048449 klebsiella			Q97fx4 clostridium	P06814 oryctolagus	Q87c65 xylella fas	Q9z196 helicobacte	7	P27951 streptococc	60	7	Q63416 rattus norv	O58221 pyrococcus	н.
SUMMARIES	OI.	GFP AEOVI	محا	PEPF MYCPU	DPOE YEAST	AC2L_HUMAN	AMPA WIGBR	ITH3 MESAU	SYL_XYLFA	D152_HAEIN	D151_HAEIN		ACS2 RHIME	STRH STRPN	CP51_CANGA	NIFD CLOPA	CAN2 HUMAN	CAN2 MACFA	SY62_DISOM	K6PF METJA	YC03 KLEPN	D153 HAEIN	SLAP BACLI	SPED_CLOAB	CAN2 RABIT	SYL_XYLFT	TRMB HELPJ	AC2L MOUSE		HKR1 YEAST	TP6B_SULSH	ITH3 RAT	LONH PYRHO	COPA_HUMAN
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ф	Query Match	97.5			6.8		•	•	6.5						٠,		٠		•		6.3	•	٠	•	•	•	•	٠	٠		•			
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Q27971 bos taurus	Oppgco ureaplasma P43367 sus scrofa P07354 rallus rall	Q80757 STEEDLOCGCC	Q9kwa3 agrobacteri
P57203 buchnera ap		Q27954 bos taurus	P58132 astasia lon
P23212 stanbulococ		P58555 anabaena sp	Q14721 homo sapien
CAN2_BOVIN	SYL UREPA	PEPX STRMU COPA_BOVIN RCA ANASP	ACSA AGRRH
HIS7_BUCAI	CANZ PIG		RPOD ASTLO
MSRA_STAEP	PIK CHICK		KCB1 HUMAN
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207	324	758	652
353		1224	817
488		414	858
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78 78 78	77.5	77.5	77 77 77
6 6 8	. E. E. E.	4 4 4	4 4 4
4 7 8		0 1 2	6 4 4

ALIGNMENTS

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=97299832; PubMed=9154981;
Rouwendal G.J.A., Mendes O., Wolbert E.J.H., de Boer A.D.;
"Enhanced expression in tobacco of the gene encoding green fluorescent protein by modification of its codon usage.";
Plant Mol. Biol. 33:989-999(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93192221; PubMed=8448132; Cody C.W., Prasher D.C., Ward W.W.; "Chemical structure of the hexapeptide chromophore of the Aequorea
                                                                                                                             Aequorea victoria (Jellyfish).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
VCBI_TaxID=6100;
                                                                                                                                                                                                                                                                                                                                                                                                                    gene and
                                                                                                                                                                                                                                                                                                  "Primary structure of the Aequorea victoria green-fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              temington S.J.;
Trystal structure of the Aequorea victoria green fluorescent
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=94185810; PubMed=8137953;
Inouye S., Tsuji F.I.;
"Aequorea green fluorescent protein. Expression of the gene fluorescence characteristics of the recombinant protein.";
ERES. Lett. 341:277-280(1994).
                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=92175527; PubMed=1347277;
Prasher D.C., Eckenrode V.K., Ward W.W., Prendergast F.G.,
Cormier M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE=98294543; PubMed=9631087;
Yang F., Moss L.G., Phillips G.N. Jr.;
"The molecular structure of green fluorescent protein.";
Nat. Biotechnol. 14:1246-1251(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X.RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE=96355665; PubMed=8703075;
<u>Ormoe M., Cubitt A.B., Kallio K., Gross L.A., Tsien R.Y.</u>
                              GFP_AEQVI STANDARD; PRT; 238 AA. P42212; Q17104; Q27903; 01-NOV-1995 (Rel. 32, Created) 1-NOV-1995 (Rel. 32, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                green-fluorescent protein.";
Biochemistry 32:1212-1218(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 273:1392-1395(1996)
                                                                                                                                                                                                                                                                                                                                 Gene 111:229-233(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHROMOPHORE
                                                                                                                                                                                                                                                                                                                    protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
RESULT 1
GFP_AEQVI
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61 VTTFSYGVQCFSRXPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                              5-imidazolinone (Ser-Gly).
2,3-DIDEHYDROTYROSINE.
F -> Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26886 MW; EASA6F21FBFB6E05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1234; DB 1; L
Pred. No. 2.3e-95;
2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                    PDB; ZEMN; Z0-AUG-97.
PDB; ZEMO; Z0-AUG-97.
InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
                                                                                                                                                                                                           97.5%;
                                                                                                                                                                3D-structure
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100
108
141
219
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20-AUG-97.
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238 AA;
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CROSSLNK
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2EMD;
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SEQUENCE
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Best Local &
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                                                                                                                                                                                                                                                                                                                      1- TISSUE SPECIFICITY: Photocytes.

1- TISSUE SPECIFICITY: Photocytes.

1- PIM: Contains a covalently attached chromophore, which is composed of modified anino acid residues. The chromophore is formed upon cyclization of the residues Ser-dehydroTyr-Gly.

1- BIOTECHNOLOGY: Has become a useful and ubiquitous tool for making chimeric proteins of GFP linked to other proteins where it functions as a fluorescent protein ed GFP tolerates N-and C-terminal fusion to a broad variety of proteins. It has been expressed in bacteria, yeast, slime mold, plants, Drosophila, zebrafish, and in mammalian cells. As a noninvasive fluorescent marker in living cells, it allows for a wide range of applications where it may function as a cell lineage tracer, reporter of gene expression, or as a measure of protein-protein interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
         X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW EMMISSION
                                                                                                                          MEDLINE-99228303 bubMed-1020315.

Bisliger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;

Bisliger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;

"Structural and spectral response of green fluorescent protein

"Structural and spectral response of green fluorescent protein

Biochemistry 38:5296-5301(1999).

-!- FUNCTION: Energy-transfer acceptor. Its role is to transduce the

blue chemiluminescence of the protein aequorin into green

Iluorescent light by energy transfer. Fluoresces in vivo upon

receiving energy from the Ca(2+)-activated photoprotein aequorin.

Absorbs light maximally at 395 nm and exhibits a smaller

absorbance peak at 470 nm. The fluorescence emission spectrum

peaks at 509 nm with a shoulder at 540 nm.
                      MEDLINE-98455509; PubMed-9782051; Wachter R.M., Elsliger M.A., Kallio K., Hanson G.T., Remington S.J.; "Structural basis of spectral shifts in the yellow-emission variants of green fluorescent protein."; Structure 6:1267-1277(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE-Issue 11 of June 2001;
WWW="http://www.expasy.org/spotlight/articles/sptlt011.html"
                                                                                                                X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
```

EMBL; M62654; AAA27722.1; -. EMBL; M62653; AAA27721.1; -. EMBL; L29345; AAA58246.1; -. EMBL; X96418; CAA65278.1; -.

1BFP; 17-NOV-00. 1C4F; 14-JUN-00. 1EMA; 08-NOV-96

JS0692; JQ1514.

1EMB; 16-JUN-97. 1EMC; 20-AUG-97. 1EME; 20-AUG-97.

12-MAY-99

1EMF; 1EMG; 1EMK; 1EML; 1EML;

20-AUG-97 17-NOV-00

LF09; LF0B;

1GFL; 1HCJ; 1HUY; 1JBY;

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Gaps

9 9

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Matches RESULT 4 οp ð à 셤 à d à This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). Ŋ, 133 ----GNILGHKL---EYNFISHNVYITADKQKN--GIKANFKI 167 73 181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238 Marture 40:105-1080(2000).

-!- FUNCTION: Catalyzes the formation of 5-methyl-uridine at position 54 (M-5-U54) in all tRNA (By similarity)
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-homocysteine + tRNA containing thymine.
-!- SIMILARITY: Belongs to the RNA M5U methyltransferase family. TrmA 79 KRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKF--EGDTLV------NRIELKG 74 IDFADEKICAFMPRLLEYLRQDNKLKEKLFGVEFLTTKQELSITLLYHKNIEDIKSNLEN STRAIN=NCTC 11168,
MEDLINE=20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.,
"The genome sequence of the food-borne pathogen Campylobacter jejuni 14 EKHSFIKKYFKBFYTKDFKLFASKDKHYRTRAELSFYHENDTLFYAMFDDFKSKKKYIIEY 31; Gaps Campylobacter jejuni. Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) tRNA (Uracall-5-)-methyltransferase (EC 2.1.1.35) (tRNA(M-5-U54).methyltransferase) 6.9%; Score 87.5; DB 1; Length 357; 26.6%; Pred. No. 4.4; tive 18; Mismatches 42; Indels 3 BY SIMILARITY. CEC5328347CEE497 CRC64; 357 AA reveals hypervariable sequences."; Nature 403:665-668(2000). Campylobacteraceae; Campylobacter HAMAP; MF 01011; -; 1. InterPro; IPR000051; SAM bind. InterPro; IPR001566; TrmA. EMBL; AL139076; CAB73096.1; -. 315 B 42276 MW; Conservative STANDARD; G81355; G81355. 315 3 357 AA; Query Match Best Local Similarity 128 IDFKED----SEQUENCE FROM N.A. 168 RHNI 171 134 LSNI 137 NCBI_TaxID=197; TRMA OR CJ0831C subfamily. TRMA CAMJE 09PP92; 33; ACT SITE SEQUENCE g à 셤 8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 --LKGIDFKEDGNILGHKLEYNFISHNVYI-TADKQKNGIKANFKIRH-----NIEDGSV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 QLADHYQQNTPIGDGPVLLPDNHYLSTQSALS-----KDPKEKRDHMVLLEFVTAAG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 SXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIE
                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of the murine respiratory pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL445507,
PIR; A99552, A99552.
MypuList; MYPU 3210;
InterPro; IRR006025; Pept M Zn BS.
InterPro; IRR001567; Peptidase M3.
InterPro; IRR0142; Peptidase M3; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Mstalloprotease; Zinc; Complete proteome.
395 ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                    Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
                                                                                                                                                                                                                                                                                                                                MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galis
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY)
ZINC (CATALYTIC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 6.9%; Score 87.5; DB 1; Length 613; Best Local Similarity 22.6%; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3504AA247096FAF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUTCHIC ACIGS Res. 29:2145-2153 (2001).
-- COFACTOR: Binds 1 zinc ion (By similarity).
-- SIMILARITY: Belongs to peptidase family M3.
                                                   16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Oligoendopeptidase F homolog (EC 3.4.24.-).
PEPF OR MYPU_3210.
        613 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2222 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 ITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasma pulmonis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: | ||||
163 VSRGNIELYK 172
                                                                                                                                                            PEPF OR MYPU 3210.
Mycoplasma pulmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       613 AA;
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                               NCBI TaxID=2107;
                                                                                                                                                                                                                                                                                                                STRAIN-UAB CTIP
                                                16-OCT-2001
16-OCT-2001
PEPF MYCPU
Q98QP0;
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ID DPOE YEAST
AC P21951;
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METAL
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us-10-057-505-2-copy.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: CONSISTS OF FIVE SUBUNITS (200 kDa, 80 kDa, 34 kDa, 30 kDa, AND 29 kDa)
-!- SUBUNIT: CONSISTS OF FIVE SUBUNITS (200 kDa, 80 kDa, 34 kDa, 30 kDa, AND 29 kDa)
-!- SUBCELLUIAN LOCATION: NUCLEAR.
-!- DOWAIN: THE DAM POLYMERASE ACTIVITY DOMAIN RESIDES IN THE N-TERMINAL HALF OF THE PROTEIN, WHILE THE C-TERMINUS IS NECESSARY FOR COMPLEXING SUBUNITS B AND C.
-!- MISCELLANEOUS: In eukaryotes there are five DNA polymerases: alpha, beta, gamma, delta, and epsilon which are responsible for different reactions of DNA synthesis.
-!- SIMILARITY: Belongs to the DNA polymerase type-B family.
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96110631; PubMed=8740425; Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.; Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.; "The sequence of a 24,152 bp segment from the left arm of chromosome XIV from Saccharomyces cerevisiae between the BNI1 and the POL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "DNA polymerase II, the probable homolog of mammalian DNA polymerase epsilon, replicates chromosomal DNA in the yeast Saccharomyces
                                                                                                                                         Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBO J. 11:733-740(1992).
-!- FUNCTION: DNA POLYMERASE II PARTICIPATES IN CHROMOSOMAL DNA
REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Araki H., Ropp P.A., Johnson A.L., Johnston L.H., Morrison A.,
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DNA polymerase epsilon, catalytic subunit A (EC 2.7.7.7) (DNA polymerase I subunit A).
POLZ OR DUNZ OR YNLZ62W OR N0825.
                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 1214-1221.
MEDLINE=90381771; PubMed=2169349;
MORTISON A., Araki H., Clark A.B., Hamatake R.K., Sugino A.;
"A third assential DNA polymerase in S. cerevisiae.";
Cell 62:1143-1151(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PR00136; DNA pol B; 1.
Pfam; PR03104; DNA pol B; 1.
SMART; SM00486; PolEs; 1.
PROSITE; PS00116; DNA POLYMERASE B; FALSE NEG.
Transferase; DNA-directed DNA polymerase; DNA replication; DNA-binding; Zinc-finger; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGD: S000206; POLZ.
GO; GO:0000731; P:DNA repair synthesis; IMP.
InterPro; IPR066172; DNA_pol_B.
InterPro; IPR066134; DNA_pol_B dom.
InterPro; IPR066133; DNA_pol_B exo.
                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEMPERATURE SENSITIVE MUTANTS.
MEDLINE=92164663; PubMed=1537345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M60416; AAA88711.1; -.
EMBL; X92494; CAA63235.1; -.
EMBL; Z71538; CAA96169.1; -.
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-2221 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A36028; A36028.
GermOnline; 143268; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (east 12:505-514(1996)
                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S288c / FY1679
                                                                                                                                                                                    NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DNA) (N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugino A.;
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REDILINE-21638749; PubMed=11780052;

RX MEDLINE-21638749; PubMed=11780052;

RA DeJOUKARS P., Matchews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Bailey J., Barlow K.F., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Basley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,

RA Chagpan J.C., Clamp M., Clark G., Clark L.M., Clark S.Y., Clee C.M.,

RA Chagp S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

Coulson A.C., Frankland J.A., Fraser A., French L., Garner P.,

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA Huckle B., Hunt A.R., Hunt S.E., Jekosech K., Johnson D.,

RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramssy H.,

RA Swann R.M., Sycanore N.T., Scoderlund C., Steward C.A., Sulston J.E.,

RA Flace C.M., Sycanore N.T., Scott C.E., Schira H.K., Showkeen R., Sims S.,

RA Fracey A., Tromans A.C., Vaudin M., Wallis J.M.,

Mitchead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

Whitchead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

Whitchead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

Whore N. W. A., Hubbard T., Durbin R.M., Bentley D.R., St.,
                                                                                                                                                   7;
                                                                                                                                                                                                                                   942
                                                                                                                                                                                                                                                                      99 FFKDDGNYKTR--AEVKFEGDTLVNR-----IELKGIDFKEDGNILGHKLEYNFI 146
                                                                                                                                                                                                                                                                                                98
                                                                                                                                                                                     53 LPVPWP-TLVTTFSXGVQCFSRYPDHM~-----KRHDFFKSAMPEGYV----QERTI
                                                                                                                                                                                                                          883 LPKSFPETYFFTLENGKKLYLSYPCSMLNYRVHQKFTNHQYQELKDPLNYIYETHSENTI
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
TISSUB=Brain, and Testis;
MEDLINE=2238625; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                   31;
                                                                                                       DB 1; Length 2222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC2L HUMAN STANDARD; PRT; 689 AA.
Q9NUB1; Q81V99; Q8N234; Q96J11; Q96JX6; Q9NU28;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amoration update)
Acetyl-coenzyme A synthetase 2-like, mitochondrial precursor (EC. 6.2.1.1) (Acetate--CoA ligase 2) (Acetyl-CoA synthetase 2)
  81 POTENTIAL.
44 M -> I (IN POL2-9 TS MUTANT).
10 P -> S (IN POL2-18 TS MUTANT)
255669 MW, CHCDDE2AB147D65B CRC64;
                                                                                                                                                 50; Indels
                                                                                                                                                 13; Mismatches
                                                                                                                             Pred. No. 56;
                                                                                                       6.8%; Score 85.5;
                                                                                                                         28.2%;
                                                                                                                    Local Similarior
hes 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           1000 SDIFKVFLEGD 1010
                                                                                                                                                                                                                                                                                                                                                    147 S--HNVYITAD 155
  2181
644
710
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                                                            2222 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAS2L OR KIAA1846
  2108
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ZN FING
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                                                                                                       Query Match
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S. Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Hellon B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Miting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Placenta, and Tonque;
A Ninomiya K., Wagatsuma M., Kahda K., Kondo H., Yokoi T., Kodaira H.,
Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
A Furuya T., Takahashi M., Yamazaki M., Irie R., Sato H.,
A Kamra K., Yamashita H., Marsuo K., Nakamura Y., Sekine M.,
A Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
A Kikuchi H., Murakawa K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
Kakuchi H., Murakawa K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
Rikuchi H., Murakawa K., Sugiyama T., Otsuki T., Ishibashi T.,
Pujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S.,
Nawai Y., Wakamatsu A., Kanehori K., Suzuki Y., Sugano S.,
Nagahari K., Masuho Y., Nagai K., Isogai T.,
NEDO human cDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for large proteins in vitro.",
DNA Res. 8:85-95(2001).
-!- FUNCTION: Converts acetate to acetyl-CoA so that it can be used
for oxidation through the tricarboxylic cycle to produce ATP and
CO(2) (By similarity).
-!- CATALYTIC ACTIVITY: ATP + acetate + CoA = AMP + diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21245130; PubMed=11347906;
Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XX.
The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 169-689 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9NUB1-2; Sequence=VSP 007249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 336-689 FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q9NUB1-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rissum=Brain;
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acetyl-CoA.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
-!- ALTERNATIVE PRODUCTS:

Note=No experimental confirmation available,

Lamily.
-!- CAUTION: Ref.1 (CAB81884) sequence differs from that shown due to erroneous gene model prediction.
-!- CAUTION: Ref.3 sequence differs from that shown due to a frameshift in position 250 and numerous sequencing errors.

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EMBL; AL035661; CAB75500.1; -.
EMBL; AL080312; CAB81884.1; ALT_SEQ.
EMBL; BC039261; AAH39261.1; -.
EMBL; BC044588; AAH44588.1; -.
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510 68 VQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRA---EVKFEGDTLVNRIE 124 8 FIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTFSXG Gaps MITOCHONDRION (POTENTIAL).
ACETYL-COENZYME A SYNTHETASE 2-LIKE. 52; EMBL; AK027817; BABS5390.1; ALT INIT.
EMBL; AK022295; BAC03853.1; ALT_SEQ.
EMBL; AK082295; BAAC03853.1; ALT_SEQ.
EMBL; AB081749; BAB4745.1; -..
InterPro; IPR000873; AMP-bind.
Pfam; PR0501; AMP-binding; 1.
PROSITE; PS00455; AMP_BINDING; 1.
Ingase; Mitochonding; Transit peptide; Alternative splicing.
TRANSIT 6.7%; Score 85; DB 1; Length 689; /FTId=VSP_007249.

777 V -> M (IN REF. 2; AAH39261).

188 V -> M (IN REF. 2; AAH44588).

74856 MW, 66E84E39302AD08B CRC64; 15; Mismatches 37; Indels Missing (in isoform 2). /FIId=VSP_007249. Pred. No. 15: POLY-ALA. 125 LKGIDFKEDGNILGHKL 141 554 -----NISGHRL 560 24.1%; 33; Conservative 36 689 53 447 689 AA; Local Similarity 446 511 CONFLICT VARSPLIC Query Match CONFLICT DOMAIN CHAIN Matches à à 셤 d à

10-OCT-2003 (Rel. 42, Last annotation update)
Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase) 501 AA. Last sequence update) 10-0CT-2003 (Rel. 42, Created) 10-0CT-2003 (Rel. 42, Last seq 10-0CT-2003 (Rel. 42, Last anno STANDARD; AMPA WIGBR Q8D295; AMPA_WIGBR RESULT

(LAP) (Leucyl aminopeptidase). PEPA OR WIGBR4590.

SEQUENCE FROM N.A. MEDILNE=22297718; PubMed=12219091; Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M., Aksoy S.; Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Wigglesworthia. "Genome sequence of the endocellular obligate symbiont of tsetse flies, Wigglesworthia glossinidia."; Nat. Genet. 32:402-407(2002). Wigglesworthia glossinidia brevipalpis. NCBI_TaxID=36870;

similarity).

-!- CATALYIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|Xbb-, in which Xaa is preferably Leu, but may be other amino acids
including Pro although not Argor Lys, and Xbb may be Pro-!- COFACTOR: Binds 2 manganese ions per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to peptidase family M17. -:- FUNCTION: Presumably involved in the processing and regular turnover of intracellular proteins. Catalyzes the removal of unsubstituted N-terminal amino acids from various peptides (By

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us-10-057-505-2-copy.rsp

SYNTHESIS AND DEGRADATION

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LOCALIZATION,
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                                                                                                                                                                                                                                                                                                                                                                                             254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
"Molecular cloning and sequencing of cDNAs encoding three heavy-chain
precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:
implications for the evolution of the inter-alpha-trypsin inhibitor
heavy chain family.";
                                                                                                                                                                                                                                                                                                                                                                                                                183 QONTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAA--GITHGMDEL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                     255 NENKFNGKSPIILIGKGLTFDSGGISIKPSNNMDEMKFDMCGAAAVLGVMHAISEL 310
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamamoto T., Yamamoto K., Sinohara H.;
"Inter-alpha-trypsin inhibitor and its related proteins in Syrian hamster urine and plasma.";
J. Biochem. 120:145-152(1996).
-!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FBB-2003 (Rel. 41, Last amoutation update)
Inter-alpha-trypsin inhibitor heavy chain H3 precursor (III heavy chain H3) (Inter-alpha-inhibitor heavy chain H3) (Hter-alpha-inhibitor heavy chain 3) (HC3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                       68; Indels 49;
                                                                                                                                                                MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
4E181EEBEB481FE3 CRC64;
                                                                                                                                                                                                                                                              DB 1; Length 501;
                                                                                                                               Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 31-50; 446-472 AND 504-523, AND SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                               151 YITADKQKNGIKANFKIRHNIEDGSVQLADH-------
                                                                                                                                                                                                                                                          6.7%; Score 84.5; DB
21.0%; Pred. No. 12;
live 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            886 AA
                                  HAMAP; MF_00181; -; 1....,
InterPro; IPR008019; Peptidase_M17_C.
InterPro; IPR00823; Peptidase_M17_N.
Pfam; PF02789; Peptidase_M17, 1.
PFam; PF02789; Peptidase_M17, 1.
PRIMT; PR00481; LAMNOPFIDASE.
PROSITE; PS00631; CYTOSOL AP; 1.
Hydrolase; Aminopeptidase; Manganese; Co
send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mesocricetus auratus (Golden hamster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97420688; PubMed=9276673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97018241; PubMed=8864857;
                         EMBL; AB063522; BAC24605.1; -.
                                                                                                                                                                                                                                   56643 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. 122:71-82(1997).
                                                                                                                                                                                                                                                                      Local Similarity 21.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                       208 YILKDKYSEKİ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10036;
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P97280;
                                                                                                                                        ACT SITE
ACT SITE
METAL
                                                                                                                                                                                                                                                                                                            92
                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 LKGID--FKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHY 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 YPDHMKRHDFFKSAMPEGYVQERT----IFFKDDGNYKTRAEVKFEGD----TLVNRIE
                                                           SUBUNIT: I-alpha-I plasma protease inhibitors are assembled from one or two heavy chains (H1, H2 or H3) and one light chain, bikumin. Inter-alpha-inhibitor (I-alpha-I) is composed of H1, H2 and bikumin, inter-alpha-like inhibitor (I-alpha-L1) of H2 and blkumin, and pre-alpha-inhibitor (P-alpha-I) of H3 and bry: PTM: Heavy chains are interlinked with bikumin via a chondroitin 4-sulfate bridge to the their C-terminal aspartate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
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N-LINKED (GLCNAC. . .) (POTENTIAL).
CHONDROITIN 4-SULFATE, CROSS-LINK SITE
(BY SIMILARITY).
  WHICH ARE
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Leucyl-trnA synthetase (EC 6.1.1.4) (Leucine--trnA ligase) (LeuRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
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Xanthomonadaceae, Xylella.
NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serine protease inhibitor; Repeat; Signal; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 886;
HYALURONAN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62; Indels
                ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES
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  Q
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                                                                                                                                                                                                                       similarity).
SIMILARITY: Belongs to the ITIH family.
SIMILARITY: Contains 1 VWFA domain.
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; Pred. No. 23;
33; Mismatches
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InterPro; IPR006587; VIT.
InterPro; IPR002035; VWF_A.
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SMART; SM00609; VIT; 1.
SMART; SM00327; VWA; 1.
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Xylella fastidiosa.
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                                           SIMILARITY)
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SIGNAL
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Q9PBG8;
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CARBOHYD
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AC 19960
DT 16-0C
DT 16-0C
DT 28-FE
DE LEUC
GN LEUC
CO Bacte
OC Manch
OX NCBI
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153 TADKQKNGIKANFKIRHNIEDGSVQLADHYQQNTPI.-
                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=727;
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                                                                                                                                                                                                                                                                                                                             D152 HAEIN
P44935;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EMCONDERING STREET INSTITUTE. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                              ARALNE-20365177; PubMed=10910347;

RA Alvarenga R., Alves L.M.C., Arruda P., Abreu F.A., Acencio M., Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Simpson A.J.G., Reinach F.C., Arruda P., Baia G.S., Baptista C.S., A Barros M.H., Barnose M.R.S., Bueno M.R.P., Camargo A.A., Camargo J.B., Bove J.M., Garrer H., R.A. Bueno M.R.P., Calombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Colduto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Arranga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., R.A. Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., R.A. Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., R.A. Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.C., Hohelsel J.D., Jungueira M.H., Kemper E.L., Kitajima J.P., R.A. Fraga J.S., Madeira A.M.B.N., Madeira H.M.F., Marino C.L., Marino C.L., Marino G.L., Abachada M.A., Mascimento A.L.T.O., Netto L.B.S., Nebarto P.G., Rodingues V., de Rosa A.J. M., Ge Oliveira R.C., Palmieri D.A., Paris A., Peixoto B.R., Pereira G.G., Pereira H.A. Ju., Pasquero J.B., Ge Souza A.C., Ge Sa R.G., Santelli R.V., Sawasaki H.E., de Souza A.P., Terenzi M.F., Truffi D., Tsai, Ge Souza A.R., Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Allada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Allada M., Marine G. Lennia, M. W., Verjovski-Almeida S., Vettore A.L., Allada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Allada M. Marine 406.111-159(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNFISHNVYI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP, MF 00049; --; 1.
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR001302; LRNA-synt 1.
InterPro; IPR001412; LRNA-synt 1.
InterPro; IPR001412; LRNA-synt 1.
InterPro; IPR00908; ValRS_ILERS_edit.
PHAM; PR00185; TRNASYNTHLEU.
IIGRFAMS; TIGR00396; leub_bact; 1.
PROSITE; PS00178; AA_TRNA_LIGASE 1; 1.
PROSITE; PS00178; AA_TRNA_LIGASE 1; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNEQLPV-WVANFVLMAYGTGAVMAVPGHDQRDQEF--ANKYGLPIRQVIALKEPKNQDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP + diphosphate + L-leucyl-tRNA(Leu).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 879;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
9FDCCB992092919E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.5%; Score 82.5; I 20.8%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE004031; AAF84975.1; ALT_INIT.
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Best Local Similarity 20.88
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641
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                              FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              637
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--GDGPVLLPDN- 198
                                          --NTPIGDGPVL 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 IFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH-----KLEYNFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Relachmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKerlavage A.R., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., McKerney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ag) (Outer membrane protein D15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 19 POTENTIAL.
20 795 PROTECTIVE SURFACE ANTIGEN D15.
795 AA; 87478 MW; B85691FC22E6ED44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: Belongs to the surface antigen D15 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 6.5%; Score 82; DB 1; Length 795; Best Local Similarity 25.0%; Pred. No. 32; Matches 40; Conservative 22; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 SHNVYITADKQK-NGIKANFKIRHNIEDGSVQLADHYQQ-----
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Pfam; PF01103; Bac surface Ag; I.
Antigen; Outer membrane; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                     795 AA
                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                   199 HYLSTQSALSKDPKEKR 215
                                                                                                                                                                                 : | | : ||: 476 AFSGTGSPIKTDPEWRK 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
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SET7 HUMAN
                                          RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Minna / Serotype B, and Eagan / Serotype B, MEDLINE=97427952; PubMed=9284140; Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Outer membrane protein D15 is conserved among Haemophilus influenzae species and may represent a universal protective antigen against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flack F.S., Loosmore S., Chong P., Thomas W.R.; "The sequencing of the 80-kDa D15 protective surface antigen of Haemophius influenzae."; ene 156:97-99(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ag) (Outer membrane protein D15).
Bacteria; Proteobacteria; Gammaproteobacteria; Proteobacteria; Pasteurellaceae; Haemophilus ind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 797 PROTECTIVE SURFACE ANTIGEN D15. 797 AA; 87675 MW; 2F93DE538696AF1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: Belongs to the surface antigen D15 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 797; 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 IFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH----
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593 IPGSDNKYYKLSADVQGFYPLDRDHLWVVSAKASAGYANG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 LP--DNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHG 232
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                                                                                                                                                                                            797 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.5%; Score 82; DB 25.0%; Pred. No. 32; ative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL. PROTECTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; JC4078; JC4078.

InterPro; IPR00184; Bac_BurfAg_D15.
Pfam; PF01103; Bac_Burface_Ag; 1.
Antigen; Outer membrane; Signal.
1 19 POTENTIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Invasive disease.";
Infect. Immun. 65:3701-3707(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Serotype B;
MEDLINE=95255676; Pubmed=7737523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U13961; AAA85645.1; -. EMBL; U60832; AAB61974.1; -. EMBL; U60833; AAB61976.1; -.
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                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI TaxID=727;
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STRAIN=Minna /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein M.H.;
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                                                                                                                                                                                     D151 HAEIN
P46024;
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                                593
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lysine-4 specific (EC 2.1.1.43)
                                                                                                                                                                                                                                                                                                                                                       Wang H., Cao R., Xia L., Erdjument-Bromage H., Borchers C., Tempst P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XIX. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., SEQUENCE OF 35-44; 108-115; 144-152; 234-258 AND 345-358, AND MUTAGENESIS OF HIS-297.
                                                                                                                                                                                                                                                                                                                                                                         Zhang Y.;
"Purification and functional characterization of a histone H3-lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21838688; PubMed=11850410; Nishloka K., Chuikov S., Sarma K., Erdjument-Bromage H., Allis C.D., Nishloka K., Chuikov S., Sarma K., Erdjument-Bromage H., Allis C.D., Tempst P., Reinberg D.; Setty a novel histone H3 methyltransferase that facilitates transcription by precluding histone tail modifications required for the terrochromatin formation."; Genes Dev. 16:479-489(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., SEQUENCE OF 36-45; 104-115; 144-152; 159-169; 201-250 AND 324-358, AND MUTAGENESIS OF HIS-297.
TISSUE-Cervical carcinoma;
                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo
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MEDLINE-22401621; PubMed=12514135;
Kwon T., Chang J.H., Kwak E., Lee C.W., Joachimiak A., Kim Y.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22259601; PubMed=12372304;
Wilson J., Jing C., Walker P., Martin S., Howell S., Blackburn
Gamblin S., Xiao B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22289682; Pubmed=12389038; Jacobs S.A., Harp J.M., Devarakonda S., Kim Y., Rastinejad F., Khorasanizadeh S.; "The active site of the SET domain is constructed on a knot."; Nat. Struct. Biol. 9:833-838(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.75 ANGSTROMS) OF 108-366.
MEDLINE=22459284; PubMed=12540855;
Xiao B., Jing C., Wilson J.R., Walker P.A., Vasisht N., Kelly Howell S., Taylor I.A., Blackburn G.M., Gamblin S.J.;
"Structure and catalytic mechanism of the human histone methyltransferase SET7/9.";
                                                                                                                   (SET domain-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Crystal structure and functional analysis of the histone
            Q8WTS6; Q9COE6; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Histone-lysine N-methyltransferase, H3 lysine-4 sg (H1stone H3-K4 methyltransferase) (H3-K4-HWIase) containing protein 7) (Set9) (SET7/9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 52-344.
    366 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21082932; PubMed=11214970;
                                                                                                                                                                                                                                                                                                                                MEDLINE=21638669; PubMed=11779497;
                                                                                                                                                                                                                                                                                                                                                                                                                 4-specific methyltransferase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Cell 8:1207-1217(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   methyltransferase SET7/9.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JNA Res. 7:347-355 (2000).
STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell 111:105-105(2002)
                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                rissum=Brain;
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RHIME
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                                                                                                                                           092KX2;
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                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 RYPDHMKRHDFFKSA-------MPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 LMPGNSVYH-FDKSTSSCISTNALLPDPYESERV-----YVAESLISSAGEGLFSKV 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 VELDGDVNGHKFSVSGEGEGDATYGKLTLKFI---CTTGKLPVPWPTLVTTFSXGVQCFS 72
                                                                                   Lee J., Cho Y.;
"Mechanism of histone lysine methyl transfer revealed by the structure of SET7/9-AdoMet.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00317; SET; 1.
PROSITE; PS50280; SET; 1.
Transferase, Methyltransferase; Chromatin regulator; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0018024; F.histone-lysine N-methyltransferase activity; NAS. GO:0016568; P:chromatin modification; NAS. InterPro; IPR003499; MORN.
InterPro; IPR001241; SFT.
Pfam; PF02493; MORN; 3.
Pfam; PF00856; SFT; 1.
SMART; SM00317; SET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 LEYNFISHNVYITADKOKNG-IKANFKIRHNIEDGSVQLADHYQQNTPIGDGP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H->A,G: ABOLISHES METHYLTRANSFERASE ACTIVITY.
                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the histone-lysine methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.4%; Score 81; DB 1; Length 366; 22.3%; Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73A1217079E3BA13 CRC64;
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                                                                                                                                                                                                                                                                                  -!- SIMILÂRITY: Contains 3 MORN repeats.
-!- SIMILARITY: Contains 1 SET domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF462150; AAL69901.1; -. AB051504; BAB21808.1; ALT_INIT.
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MORN 2.
MORN 3.
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                                                       /9-AdoMet.";
22:292-303(2003)
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1MUF; 06-NOV-02.

1N6A; 04-FEB-03.

1N6C; 04-FEB-03.

109S; 06-FEB-03.
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nes 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    606594;
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Matches
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MIM;
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PDB;
              RATERIAN AND BEAR AND
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                                                                                                                                                                                                                             10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Acetyl-coenzyme A synthetase 2 (BC 6.2.1.1) (Acetate--CoA ligase 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=1021;
MEDLINE-21396507; PubMed=11481430;
MEDLINE-21396507; PubMed=11481430;
Gapela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Waidner S., Galibert F.,
"Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium mellioti strain 1021 ",
Proc. Natl. Acad. Sci. US.A. 98:9877-9882(2001).
295 ANHSFTPNCIYDMFVHPRFGPIKCIRTLRAVEADEELTVAYGYDHSPPGKSGP 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acetyl-CoA.
PTM: Acetylated. Deacetylation by the SIR2-homolog deacetylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activates the enzyme (By similarity).
SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
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ACSA2 OR R03327 OR SMC04093.
Rhizobium melliloti (Sinorhizobium melliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 6.4%; Score 81; DB 1; Length 649; Local Similarity 25.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACETYLATION (BY SIMILARITY).
ACC3ED95B87BAC92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             502 CRRDEDGYYWIIGRVDDVLNVSGHRLGIAEVESALVSHNL 541
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                                                                                                                                                                        649 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
PRINTG; PR00154; AMPBINDING.
Ligase; Acetylation; Complete proteome.
ACT_SITE

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AL591793; CAC47906.1; -.
HAMAP; MF 01123; -: 1.
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                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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RESULT 13

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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=2001-L5;
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                                                                                                                                                                                                                                                                                                                                          MEDLINE=2137209; PubMed=11463916;
MEDLINE=2137209; PubMed=11463916;
MEDLINE=2137209; PubMed=11463916;
Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Holtzapple B., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                        STRAIN=ATCC 12213;
MEDLINE=95238375; PubMed=7721787;
Clarke V.A., Platt N., Butters T.D.;
Cloning and expression of the beta-N-acetylglucosaminidase gene from Streptococcus pneumoniae. Generation of truncated enzymes with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing N-acetyl-D-hexosamine residues in N-acetyl-beta-D-hexosaminides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REMOVED BY SORTASE (POTENTIAL).
CATALYTIC DOMAIN 1.
CATALYTIC DOMAIN 2.
LPXTG SORTING SIGNAL (POTENTIAL).
AMIDE-LINKED TO CELL WALL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001540; Glyco hydro 20.
InterPro; IPR005877; Gpos YSIRK.
InterPro; IPR005899; Gram pos anchor.
InterPro; IPR00728; Glyco hydro 20; 1.
Pfam; PF00746; Gram pos anchor; 1.
Pfam; PF04650; YSIRK signal; 1.
IIGRPAMS; TIGR01167; LEXTRC anchor; 1.
IIGRPAMS; TIGR01168; YSIRK signal; 1.
IIGRPAMS; TIGR01168; YSIRK signal; 1.
PROSITE; PS50847; GRAM POS ANCHORING; 1.
Hydrolase; Glycosidase; Cell wall; Peptidoglycan-anchor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to family 20 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BETA-N-ACETYLHEXOSAMINIDASE
                                                                                                                              Bactēria; Firmīcutes; Lactobacillales; Streptococcaceae;
                                                    16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Beta-N-acetylhexosaminidase precursor (EC 3.2.1.52)
            PRT; 1312 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                    modified aglycon specificity.";
J. Biol. Chem. 270:8805-8814(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L36923; AAC41450.1; -.
EMBL; AE007323; AAK74246.1; -.
PIR; A56390; A56390.
PIR; E95006.
TIGR; SP0057; -.
                                        (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an amide bond (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 293:498-506(2001)
                                                                                                                   Streptococcus pneumoniae
         STANDARD;
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                           NCBI_TaxID=1313;
                                                                                                   STRH OR SP0057.
                                      01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pneumoniae.
         STRH STRPN
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                                                                                                                                                                                                                                                                                                                                                                                                                             101 KDDGNYKTRAEVKFEGDTLVNRIE--LKGIDFKEDGNILGHKLEYNFISHNVYITADKQK 158
                                                                                                                                                                                                                                                                                                         896 NTNGDWYYILGQKPEDG--GGFLKKAIENTGKTPFNQLASTKYPEVDLPTVGSMLSIWAD 953
                                                                                                                                                                                                                                                                                                                                                  NGIKANFKIRHNI----EDGSVQLADHYQQNTPIGDGPVLLPD----NHYLSTQSALSK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Geber A., Hitchcock C.A., Swartz J.E., Pullen F.S., Marsden K.E., Kwon-Chung K.J., Bennett J.E., "Deletion of the Candida glabrata ERG3 and ERG11 genes: effect on cell viability, cell growth, sterol composition, and antifungal susceptibility.";
                                                                                                                                                                                                                                                                        ----VPWPTLVTTFSXGV-
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Rapid detection and identification of Candida albicans and Torulopsis (Candida) glabrata in clinical specimens by species-specific nested PCR amplification of a cytochrome P-450 lanosterol-alpha-demethylase (L1A1) gene fragment.", J. Clin. Microbiol. 32:1902-1907(1994).

-!- FUNCTION: Catalyzes C14-demethylation of lanosterol which is critical for ergosterol biosynthesis. It transforms lanosterol into 4,4'-dimethyl cholesta-8,14,24-triene-3-beta-ol (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CP51_CANGA STANDARD; PRT; 533 AA.
P50859; Q02312;
10.0CT-1996 (Rel. 34, Last sequence update)
10.0CT-2003 (Rel. 42, Last annocation update)
10.0CT-2005 (Rel. 42, Last annocation update)
24ycochrome P450 51 (RC 1.14.13.70) (CYPLI) (P450-LIA1) (Sterol 14-lapha-demethylase) (Lanosterol 14-alpha demethylase) (P450-14DM).

BRG11 OR CYPSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burgener-Kairuz P., Zuber J.P., Jaunin P., Buchman T.G., Bille J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Candida glabrata (Yeast) (Torulopsis glabrata).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                  78;
                                                                                                                                                                                           Score 81; DB 1; Length 1312;
Pred. No. 71;
                                  A -> E (IN REF. 1).
Q -> L (IN REF. 1).
V -> A (IN REF. 1).
E -> K (IN REF. 1).
C -> R (IN REF. 1).
V -> A (IN REF. 1).
V -> A (IN REF. 1).
WW, 503375B5257A90B5 CRC64;
                                                                                                                                                                                                                               36; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrob. Agents Chemother. 39:2708-2717(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1114 TTETVLDSQVTKEVINQVVEVGAPVTHKGDE 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235
                                                                                                                                                                                                                                                                      21 DVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 DPKEKRDHMVLLEFV----TAAGITHGMDE
  MISSING
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E E E I
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                                                                                                                                                      144549 MW;
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                                                                                                                                                                                                           20.7%;
                                                                                                                                                                                                                               56; Conservative
39
69
169
617
1045
1161
1171
39 3
69 6
169 16
617 61
1045 104
1161 116
1171 1177 126
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us-10-057-505-2-copy.rsp

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MEDLINE=82030699; PubMed=7026551;
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      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                       77
                                                                                                                                                                                                                                                                                                                                                                     109 GHEFIFNAKLADVSAEAAYSHLT-----TPV-----FGKGVIYDC----PNHR
                                                                                                                                                                                                                                                    IRON (HEME AXIAL LIGAND) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                             -MKRHDFFKSAM-PEGYV-----QERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGI
                                                                                                                                                                                                                                                                                                                                                                                                                                     129 DFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQQNTPI
                                                                                                                                                                                                                                                                                                                                                  24 GHKFSVS---GEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTFSXGV--QCFSRYPDH-
                                                                                                                                                                                                                                                                                                                                53; Gaps
         CATALYTIC ACTIVITY: Obtusifoliol + 3 O(2) + 3 NADPH = 4-alphamethyl-5-alpha-ergosta-8,14,24(28)-trien-3-beta-ol + formate +
                                                                                                                                                                     EMBL; 575389; AAB32679.1; -.
InterPro; IPR001128; Cytochrome_P450.
Pfan, PP00067; p450; 1.
PRINTS; PR00385; P450.
PROSITE; P800086; CYTOCHROME_P450; 1.
Blectron transport; Oxidoreductase; Monooxygenase; Membrane; Heme; Sterol biosynthesis; NADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87231095; PubMed=3473447;
Wang S.-Z., Chen J.-S., Johnson J.L.;
"Nucleotide and deduced amino acid sequences of nifD encoding the alpha-subunit of nitrogenase More protein of Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium pasteurianum.
Bacteria, Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1988 (Rel. 07, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nitrogenase molybdenum-iron protein alpha chain (EC 1.18.6.1)
(Nitrogenase component I) (Dinitrogenase).
                                                                                                                                                                                                                                                                                                           DB 1; Length 533;
                                                                                                                                                                                                                                                                                                                               77; Indels
                                                                                                                                                                                                                                                             I -> M (IN REF. 2).
I -> T (IN REF. 2).
; A0506C17507E6EF7 CRC64;
                          MADP(+) + 3 H(2)0.
-!- PATHWAY: Ergosterol biosynthesis.
-!- SIMIDARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                        6.4%; Score 80.5; DP
22.6%; Pred. No. 27;
ive 31; Mismatches
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                                                                                                                                                                                                                                                                       473 473 I 533 AA; 61305 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
01-APR-1988 (Rel. 07, Last seg
                                                                                                                                                             EMBL; L40389; AAB02329.1; -.
                                                                                                                                                                                                                                                                                                                    22.68:
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SEQUENCE OF 1-179.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pasteurianum
                                                                                                                                                                                                                                                                                                                            47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                            78
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                                                                                                                                                                                                                                                                                                                   Local
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Matches
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NIFD_CLOPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93344379; PubMed=833705; Kim J., Woo D., Rees D.C.; AMOSIKONS).

Kim J., Woo D., Rees D.C.; AMOSIKONS).

Kim J., Woo D., Rees D.C.;

Kim J., Moo D., Rees D.C.;

Kim J., Moo D., Rees D.C.;

Biochemistry 32:7104-7115(1993).

-! FUNCTION: The key enzymatic reactions in nitrogen fixation are catalyzed by the nitrogenase complex, which has 2 components: the iron proctein and the molybdenum-iron protein.

-!- CATALYIC ACTIVITY: 8 reduced ferredoxin + 8 H(+) + N(2) + 16 ATP = 8 oxidized ferredoxin + 2 NH(3) + 16 ADP + 16 phosphate.

-!- SUBUNIT: TETRAMER OF FWO ALPHA AND TWO BETA CHAINS THAT BINDS

-!- 3UBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS THAT BINDS
Hase T., Nakano T., Matsubara H., Zumft W.G.;
"Correspondence of the larger subunit of the MoFe-protein in
clostridial nitrogenase to the nif D gene products of other N2-fixing
organisms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen K.C.K., Chen J.-S., Johnson J.L., "Structural features of multiple nifH-like sequences and very biased codon usage in nitrogenase genes of Clostridium pasteurianum."; J. Bacteriol. 166:162-172(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 525-533 FROM N.A.
MEDLINE=88294019; PubMed=2840948;
Wang S.-Z., Chen J.-S., Johnson J.L.;
"Distinct structural features of the alpha and beta subunits of nitrogenase molybdenum-iron protein of Clostridium pasteurianum: an analysis of amino acid sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00090; NITROGENASE 12; 1.
PROSITE; PS00699; NITROGENASE 11; 1.
Oxidoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur; 3D-structure.
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-!- SIMILARITY: BELONGS TO THE NIFD/NIFK/NIFE/NIFN FAMILY.
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InterPro; IPR000118; Nitrognse_compl.
InterPro; IPR000510; Oxred_nitrognsel.
Ffam; PF00148; Oxidoxed_nitro; ITGRFAMS; TIGRFAMS; T
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=86168010; PubMed=3457003;
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EMBL, Y00155, CAA68349.1, --
EMBL, M20380, AAA23265.1, --
PPR, S07389, NICLMA.
PDB, IMIO, 31-OCT-93.
                                                                                                                                                                                                                 Biochem. 90:295-298(1981)
                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-166 FROM N.A.
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9; 57 ----TIKFIC--TIGKLPVPW--Query Match
6.4%; Score 80.5; DB 1; Length 533;
Best Local Similarity 19.9%; Pred. No. 27;
Matches 48; Conservative 38; Mismatches 98; Indels 57; Gaps 17 ELDGDVNGHKFSVSGEGEGDATYGKL-----

ð g ð

-----PTLVTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNY-KTRA 110

58

283 CNFIGVDGIVETLRDWAKCFDD-PELTKR-----TEEVIAEIAAIQDDLDYFKEKL 333 111 EVK------FEGDTLVNRIELKGIDFKEDGNILGHKLEY-------NFISHN-- 149 : | : | : | | : | | 334 QGKTACL/YVGGSRSHIYMNMLKSFGVDSLVAĞFEFAHRDDYEGREVIPTIKIDADSKNIP 393 150 -VYITADKQKNGIKANFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALS 208 | : : | |: | : | : | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : | : | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : | | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 209 K 209 454 K 454 à 셤 oy P ò

Search completed: April 19, 2004, 15:06:28 Job time : 18 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

using sw model protein search, OM protein

April 19, 2004, 15:03:20 ; Search time 20 Seconds (without alignments) 1144.679 Million cell updates/sec Run on:

US-10-057-505-2-COPY
1265
1 MSKGEELFTGVVPILVELDG......VLLEFVTAAGITHGMDELYK 238 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

pir1:* pir2:* pir3:* PIR 78:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.

	Description	green-fluorescent	hypothetical prote			tRNA (uracil-5-)-m	oligoendopentidase	sterol binding pro	DNA-directed DNA p	vegetatible incomp	inter-alpha-trypsi	hypothetical prote	DNA-binding protei	hypothetical prote	ABC-type transport	iron-regulated out	leucyl-tRNA synthe	hypothetical prote	hypothetical prote	protective surface	protective surface	fibronectin-bindin	polyketide synthas	glucose dehydrogen	protein F10B6 14 [heta-N-acetylhexos	hypothetical prote	iron-sulfur offert		T
SUMMARIES	ID	JQ1514	H72228	D71614	AD2052	G81355	A99552	AE3629	A36028	AB3548	JC5576	B86815	T06586	F71620	E81317	H64708	E82590	H86201	T27856	JC4078	F64102	S42798	AI2140	B83911	F86281	E95006	T22410	E70390	NICLMA	C70031
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d	Query Match	97.1		7.2		6.9	6.9	6.9	6.8	6.7	6.7	9.9	9.9	9.9	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4
	Score	1228	96	91.5	88	87.5	87.5	87	S	84.5	84.5	84	83	m	82.5	82.5	82.5	82.5	82	85	82	82	81.5	81	81	81	80.5	80.5	80.5	80.5
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A. Molecule type: mRNA
A. Residues: 1-24, 'Q', 26-29, 'R', 31-83, 'L', 85-153, 'G', 155-156, 'P', 158-171, 'K', 173-208, 'Q', A. Residues: 1-24, 'Q', 26-29, 'R', 31-83, 'L', 85-153, 'G', 155-156, 'P', 158-171, 'K', 173-208, 'Q', A. Cross-reference: Elone gfp2
A. Cross-reference: Clone gfp2
R. Yang, F.; Moss, L.G.; Phillips Jr., G.N.
R. Yang, F.; Moss, L.G.; Phillips Jr., G.N.
A. Reference number: A65692; PDB: 1GFL
A. Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 'A', 2-79, 'R', 81-5; A; Note: engineered sequence based on JQ1514, cloned and expressed in Escherichia coli A; Note: engineered sequence based on JQ1514, cloned and expressed in Escherichia coli A; Note: Elotechnol. 14, 1246-1251, 1996
A; Note: The molecular structure of green fluorescent protein.
A; Reference number: A58953; MUID: 98294543; PMID: 9631087

calpain (EC 3.4.22	hypothetical prote	synaptogamin o-p65	hypothetical prote	ATP-dependent nucl	S-layer protein pr	hypothetical prote	S-adenosylmethioni	calpain (EC 3.4.22	hypothetical prote	hypothetical prote	probable exported	hypothetical prote	hypothetical prote	sensory transducti	IgA Fc receptor pr
CIHUH2	T39047	JH0414	C64500	C71633	JC4930	B32259	B97220	B24815	865213	B85362	AE1055	D71900	C72293	875005	A60234
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80.5	80.5	80	80	80	80	79.5	79.5	79.5	79.5	79.5	79.5	79	79	79	79
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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A;Accession: S51330
A;Molecule type: mRNA
A;Residues: 1-13,'V',15-24,'Q',26-44,'N',46-153,'G',155-156,'P',158-171,'K',173-227,'R',
A;Cross-references: EMBL:X83959; NID:g634008; PIDN:CAA58789.1; PID:g634009
                               C;Species: Aequorea victoria
C;Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text change 23-Mar-2001
C;Accession: US0692; UQ1514; PQ0335; S48693; S51330; S51331
R;Prasher, D.C.; Eckenrode, V.K.; Ward, W.W.; Prendergast, F.G.; Cormier, M.J.
Gene 111, 229-233, 1992
A;Title: Primary structure of the Aequorea victoria green-fluorescent protein.
A;Reference number: UQ1514; MUID:92175527; PMID:1347277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Molecule type: protein
A, Molecule type: protein
A, Mesidues type: protein
A, Mesidues type: protein
B, Incuye, S.; Tsuji, P. I. 22:132-151;154-183;185-200 < PRA3>
R; Incuye, S.; Tsuji, P. I. 294
R; Incuye, S.; Tsuji, P. I. 211-214, 1994
A, Title: Evidence for redox forms of the Aequorea green fluorescent protein.
A, Reference number: 848693; MUID:94364470; PMID:8082767
A, Rocession: S48693
A, Status: preliminary
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Molecule type: mRN5
A, Cross-references: GB:L29345; NID:g606383; PIDN:AAA58246.1; PID:g606384
R; Watkins, J. N.; Campbell, A.K.
A, Meference number: S51330
                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-107,'S',109-238 <PFA1>
A;Cross-references: GB:M62654; NID:g155662; PIDN:AAA27722.1; PID:g155663
A;Accession: JQ1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
XResidues: 1-99, Fr, 101-140, L',142-218, V',220-238 <PRA2>
A;Cross -references: GB:M62653; NID:g155660; PIDN:AAA27721.1; PID:g155661
A;Accession: PQ0335
green-fluorescent protein [validated] - hydromedusa (Aequorea victoria)
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A, Accession: S51331
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210 DPKEKRDHMVLLEFV 224
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237 TYLKRERDYM 246
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A,Cross-references: GB:AE001806; GB:AE000512; NID:G4962196; PIDN:AAD36691.1; PID:G498219
A,Experimental source: strain MSB8
A;Contents: annotation; X-ray crystallography, 1.9 angstroms (see PIR:AQJFNV) emittin C;Comment: This protein is excited by the photoprotein aequorin (see PIR:AQJFNV) emittin C;Comment: The chromophore of this protein is formed by modification of Ser-dehydro-Tyr-C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: H72228
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: H72228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LVRKGLLPHPYVGM-
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                              1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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0
                                                                                                                         A; Introns: 69/3; 167/3
C; Superfamily: green-fluorescent protein
C; Keywords: chromoprotein; luminescence
C; Keywords: chromoprotein; luminescence
F; 65-67/Cross-link: 5-imidazolinone (Ser-Gly) #status experimental
F; 66-6/Modified site: dehydrotyrosine (Tyr) #status experimental
                                                                                                                                                                                                                                                                                        Query Match
97.1%; Score 1228; DB 1; Length 238;
Best Local Similarity 95.8%; Pred. No. 5e-98;
Matches 228; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.6%; Score 96; DB 2; Length 785; Best Local Similarity 20.9%; Pred. No. 3.5; Matches 40; Conservative 25; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein TM1624 - Thermotoga maritima (strain MSB8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : | | : | : | : | : | | | DVYLNGVYL----KEKNHLKVYIK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 NEGRESFEGTVPGVVQAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 YQQNTPIGDGP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEONYGVLGGP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: TM1624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                        A;Gene: GFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
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hypothetical protein all1970 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AD2052
B;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Shitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ans A;Reference number: AB1807; MUID:21595285; PMID:11759840
hypothetical protein PFB0460c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Ju1-2000
C;Accession: D71614
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, B.V.;
P. Pertees, M.; Salzbergy, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-2573 «GAR»
A;Cross-references: GB:AE001396; GB:AE001362; NID:g3845188; PIDN:AAC71881.1; PID:g38451!
A;Experimental source: clone 3D7
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
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A;Residudes: L-281 «CMD»
A;Crosu-references: GB:BA000019; PIDN:BAB73669.1; PID:g17131060; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 YKTRAEVKFEGDTLVNRIELKGI----DFKEDGNILGHKLEYNFISHNVYITADKQKNGI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 KANFKI - - RHNIEDGSVQLADH-----YQQNTPIGDG----PVLLPDNHYLSTQSALSK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: D71614
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 FKARS-LOSSDILLNPIKYNNLONRPDWKKDEYYIVHAEGYKY-KHE----SSKRKHSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 VQERTIFFKD--DGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNFISH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVYITADKOKNGIKANFKIRHNIEDGSVOLADHYQQNTPIGDGPVLLPDNHYLSTQSALS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.2%; Score 91.5; D
Best Local Similarity 26.9%; Pred. No. 41;
Matches 35; Conservative 31; Mismatches
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Asholze
DNA-directed DNA polymerase (EC 2.7.7.7) II catalytic chain - yeast (Saccharomyces cerevision C)species: Saccharomyces cerevisian DNA-directed DNA polymerase II chain A; protein N0825; protein NNL26; C)species: Saccharomyces cerevision 10-Sep-1999 #text_change 21-Jul-2000 C; Accession: A36028; B36028; E60919; S63235; S65121 R; Arither A 26028; B36028; E60919; S63235; S65121 R; Arither A third essential DNA polymerase in Saccharomyces cerevisiae.

A; Title: A third essential DNA polymerase in Saccharomyces cerevisiae.

A; Accession: A36028 MUDD:90381771; PMID:2169349
A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: Drotein
A; Residues: 11-222 cMOR.
A; Accession: B36028
A; Molecule type: Drotein
A; Residues: 1214-1216; XX, 1218-1221 cMO2.
A; Accession: B36028
A; Molecule type: Drotein
A; Residues: 1214-1216; XX, 1218-1221 cMO2.
A; Accession: B36028
A; Molecule type: Drotein
A; Residues: 1214-1216; AX, 1218-1221 cMO2.
A; Residues: 1214-1216; AX, 1218-1221 cMO2.
A; Residues: 1214-1216; AX, 1218-1221 cMO2.
A; Residues: 12121-221 cSEN.
A; Residues: 1-2221 cSEN.
                                                                                                                                                                                                                                                                                                                                    sterol binding protein [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: Ol-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AB3629
R;DelYecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, F.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes: Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten: A;Accession: A53629
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      ---KDPKEKRDHMVLLEFVTAAG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 KGIDFKEDGNILGHKLEYNFISHNVYITADKOKNGIKANFKIRHNIEDGSVQL-ADHYQQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE008918; PIDN:AAL54200.1; PID:g17985169; GSPDB:GN00191
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 FSRYPDHM-KRHDFFKSAMPEGYVQE----RTIFFKDDGNYKTRAEVKFEGDTLVNRIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 FERLGEHVNKRRFGFRPSDLPFTFLVEPGKPRISVFRQDAAFE--ADAAIEGPLVMLLALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
                                          6.9%; Score 87; DB 2; Length 175; 26.8%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 AGPF--GPVVRSIAGYI-REKALGADAHDREAH 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 NTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDH 217
      177 QLADHYQQNTPIGDGPVLLPDNHYLSTQSALS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity 26.8
41; Conservative
                                                                                                                           229 ITHGMDELYK 238
                                                                                                                                                                     :: | |||||
163 VSRGNIELYK 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule_type: DNA
A;Residues: 1-173 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
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A;Gene: BMEII0958
A;Map position: II
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Matches 4
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R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Camall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel A; Kebs. 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyphyReference number: Ag1250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: A99552
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Mucleic Acids Res. 29, 2145-2153, 2001
A;Itile: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Status: preliminary
A Molecule type: DNA
A Residues: 1-357 <PAR>
A Cross-references: GB:AL139076, GB:AL111168; NID:g6968128; PIDN:CAB73096.1; PID:g696827
A Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                              Campylobacter jeju
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A;Experimental source: strain UAB CTIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --LKGIDFKEDGNILGHKLEYNFISHNVYI-TADKQKNGIKANFKIRH-----NIEDGSV 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 KRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKF--EGDTLV------NRIELKG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GNILGHKL---EYNFISHNVYITADKQKN--GIKANFKI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73
                                                                                                                                                                                     C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
                                                                                                                                                        Cj0831c [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Keywords: methyltransferase; S-adenosylmethionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.9%; Score 87.5; DE 26.6%; Pred. No. 6.8; iive 18; Mismatches
                                                                                                                                                        (EC 2.1.1.35)
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22.6%; Pred. No. 14;
:ive 38; Mismatches
                                                                                                                                                     tRNA (uracil-5-)-methyltransferase
   QQKEKLSQDKIQELV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 22.64
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-613 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 RHNI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 LSNI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 IDFKED--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: trmA; Cj0831c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: G81355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: MYPU 3210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
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inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar-1999
C;Accession: dC5576; PC4486
R;Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohara, H.
A;Ritle: Molecular 122, 71-82, 1997
A;Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors sin inhibitor heavy chain family.
A;Reference number: dC5574; MUID:97420688; PMID:9276673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: protein
A,Residues: 34-53;449-475;509-526 <NA2>
C,Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 were the complexes play important role for panceatic cancer.
C,Superfamily: inter-alpha-trypsin inhibitor complex component II
F;236-239,664-865/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.; Ehrl:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein ypgD [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: B86815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehr Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A;Reference number: A86625; WUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 LKGID--FKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHY 182
                                                                                                           131 FAPKG--ORLAIARYNGATLIWAGTAAKPVELEWKGAHIGITFSPDGRFLITSMQENALH 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 YPDHMKRHDFFKSAMPEGYVQERT----IFFKDDGNYKTRAEVKFEGD----TLVNRIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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78 VTELANIPRKWITAVATGPNGTVGFASGKTAWSRAADG-KVQEFTQERSVEG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 889;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 QONTPIGDGPVLLPDNHYLSTQSALSKDPKE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.7%; Score 84.5; D
Best Local Similarity 24.5%; Pred. No. 41;
Matches 37; Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 84; DB Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | :::: | | S93 HFVTPLTPMVVTKPEDN--EDQTSIADKPGE
                                                          100 FKDDGNYKTRAEVKFEGDTLV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.6%;
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A;Experimental source: liver
A;Accession: PC4486
                                                                                                                                                                                                                    189 GWRLEDN 195
                                                                                                                                                                   138 GHKLEYN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-889 <NAK>
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A;Molecule type: DNA
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vegetatible incompatibility protein het-e-1 [imported] - Brucella melitensis (strain 16M
                                                                                                     A; Molecule type: DNA
A; Residues: 1-222 <SENA
A; Residues: 1-222 <SENA
A; Cross-tree: 1-222 <SENA
A; Experimental source: strain S288C
K; Sen-Gupta, M; Lyck, R.; Fleig, U.; Niedenthal, R.K.; Hegemann, J.H.
R; 550-514, 1996
A; Title: The sequence of a 24 152 bp segment from the left arm of chromosome XIV from Sa
A; Reference number: S65111; MUID: 96310631; PMID: 8740425
                                                                                                                                                                                                                                                                                                                                                                                                              A)Residues: 1-2221 <SEF>
A;Cross-references: EMBL:X92494; NID:g1045236; PIDN:CAA63235.1; PID:g1045247
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           943 FFEVDGPYKAMILPSSKEEGKGIKKRYAVFNEDGSLAELKGFELKRRGEL---QLIKNFO 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPKSFPETYFFTLENGKKLYLSYPCSMLNYRVHQKFTNHQYQELKDPLNYIYETHSENTI 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --IELKGIDFKEDGNILGHKLEYNFI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Cross-references: GB:AE008918; PIDN:AAL53549.1; PID:g17984458; GSPDB:GN00191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIGGIPFFAMADGAVHRLDDGHQTSTVHDGLLSAAMAVDGKSLVTGGEDGRVCRIDAKGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CT-TGKLPVPWPTLVTT-----FSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AB3548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --KRHDFFKSAMPEGYV----QERTI
R;Sen-Gupta, M.; Lyck, R.; Niedenthal, R.K.; Fleig, U.N.; Hegemann, J.H. submitted to the Protein Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: SGD:POL2; DUN2; MIPS:YNL262w
A;Cross-references: SGD:S0005206; MIPS:YNL262w
A;Map position: 14L
C;Superfamily: DNA-directed DNA polymerase II
C;Superfamily: DNA-directed DNA polymerase; nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.8%; Score 85.5; DB 1; Length 2222; Best Local Similarity 28.2%; Pred. No. 1.1e+02; Matches 37; Conservative 13; Mismatches 50; Indels 31.
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                                                                                                                                                                                                                                                                                                                       A; Accession: S65121
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
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Pred. No. 11;
19; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDIFKVFLEGD 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 S--HNVYITAD 155
                                                             A; Reference number: S63235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
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                                                                                       A; Accession: S63235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Residues: 1-324
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Gene: BMEII0307
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A;Residues: 1-564 <PRN>
A;Residues: 1-564 <PRN>
A;Cross-references: GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB73385.1; PID:g696856
A;Cross-references: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: wlaB; Cj1130c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillir C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Cawlorg, 65-669, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp. A;Reference number: A81250; WUID:20150912; PMID:10688204
                                                                         GB:AE001362; NID:93845124; PIDN:AAC71835.1; PID:9384512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABC-type transport protein Cj1130c [imported] - Campylobacter jejuni (strain NCTC 11168)
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                                                                                                                                                                                                                                                                                                                                                                                172
                                                                                                                                                                                                                                                                                                                                                                                                                          460 NAEVKKKKNTLRKKKKKKEKKNFLNDHMKEVTKNDDDDDDDDDDDDDDNMTKVEEKOKYNDE 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 ANNTKNYRQKIGYIPQNIYLFNDSIAKNITFGDAVDEEKLNRVIKQANLE-----HF 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYVQERTIFFKDDGNYKTRAEVKFEGD-----TLVNRIELKGIDFKEDGNILGHKLEYN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 -----FISHNYITADKQKNGI-----KANFKIRH-NIEDGSVQLADHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGKENVSIDNVEECNKMKDEYDKKENNVSNIEEENIILDSKEQNIILDTNKEKLISKEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --QLADHYQQN----TPIGDGPVLL---PDNHYLST--QSALSKDPK
                                                                                                                                                                                                                                                                                     94 QERTIFFKDDGN--YKTRAE--VKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNFI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55;
                                                                                                                                                                                                                                         62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57; Indels
                                                                                                                                                                                        Length 646;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                       50;
                                                                                                                                                                                        6.6%; Score 83; DB 2;
22.4%; Pred. No. 36;
live 30; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.5%; Score 82.5; DF
25.0%; Pred. No. 33;
live 29; Mismatches
                                                                       A;Cross-references: GB:AE001381;
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0230c
                                                                                                                                                                                        Query Match
Best Local Similarity 22.4%
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 25.0%
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --MDELYK 238
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  A;Status: preliminary; 1
A;Molecule type: DNA
A;Residues: 1-646 <GAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 EKR 215
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580 KKK 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: E81317
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                                                                                                                                                                                                                                                                                                                                                                                147
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C;Species: 1919m sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C;Accession: T06586
R;Sato, N; Kazuno, A.A.; Ohta, N.; Ohshima, K.
Submitted to the EMBL Data Library, June 1996
A;Description: Identification of a novel family of DNA-binding proteins with two AT-hook
A;Reference number: Z15774
A;Accession: T06586
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-632 <&A.
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R; Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A; Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A; Reference number: A71600; MUID: 99021743; PMID: 9804551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
  13;
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                                                                                                                                                                       319 AFESKLELKNLAVAFPDGQ-----KIEYPEIVIEKGKKYAIIGDSGSGKSTLINLLVGN 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --YNFISHNVYITADKOK----N 159
                                                                                           ---EVT 318
                                                                                                                                                                                                                               111 EVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHN 170
                                                                                                                                                                                                                                                                                                                             -----DHYQQNTP---- 202
                                                                                                                                                                                                                                                                                                                                                             | | | :::|
427 IFDKSIRIACADDFVFNKLDTVYDKNLSGGQQERLSVARELMGSKPILVMDESTASVDKK 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 PDHMKRHDFFKSAMPEGYV-----QERTIFFKDDGNYKTRAEVKFEGDTLVNRIE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             468 LKGIEPTDNSTLLDEKFENALGNKILKEISNPRHDVESANHSTHNKQVTVSHQKAIETNN 527
                                                 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T06586
DNA-binding protein PD2 - garden pea
C.Specises: Pisum sativum (garden pea)
C.Species: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
                                         10 GVVPILVELDGDVNGHKFSVSGE-----GEGDATYGXLTLKFICTTGKLPVPWPTLVT
                                                                                                                                    63 TFSXGVQCFS---RYPDHMKRHDFFKSAMPEGYVQ--ERTIFFKDDGNYKTRA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL:X98740; NID:e995229; PIDN:CAA67292.1; PID:e275185
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  74;
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                                                                                      266 GVVMSVGNLSGTVTNYSKSVANSLILLNATGKLLEKYGKITDESKVTDGE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.6%; Score 83; DB 2; Length 632;
23.3%; Pred. No. 35;
tive 23; Mismatches 82; Indele
  Indels
  :96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 GIKANFKIRHNIEDG-----SVQLADHYQ 183
  43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: cv. Alaska
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 LKGIDFKEDGNILGHKLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 23.34
Matches 49; Conservative
  61; Conservative
                                                                                                                                                                                                                                                                                                                          171 IEDGSVQLA--
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Matches
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C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 29-Sep-1999
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 29-Sep-1999
C;Accession: H64708
R;Tohneb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Areference number: A64520; MUID:97394467; PMID:9252185
A;Accession: H64708
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Mesidues: 1-877 arms
A;Residues: 1-877 arms
A;Residues: 1-877 arms
A;Residues: 1-877 arms
A;Residues: 1-877 arms
A;Csuperfamily: iron-regulated outer membrane protein

115 EGDTLVNRIEL--KGIDFK-----EDGNILGHKLEYNFISHN--VYITADKQKNGIKAN 164 33; Gaps Query Match 6.5%; Score 82.5; DB 2; Length 877; Best Local Similarity 35.3%; Pred. No. 59; Matches 36; Conservative 7; Mismatches 26; Indels 33

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165 FKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSA 206 | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 510

Search completed: April 19, 2004, 15:07:59 Job time : 21 secs

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April 19, 2004, 15:07:31; Search time 47 Seconds (without alignments) 1395.962 Million cell updates/sec
                                                                                                                                                                                                                                                        US-10-057-505-2-COPY
1265
1 MSKGEELFTGVVPILVELDG......VLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
3: cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
7: cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
8: cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
9: cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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18: cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                          1124875 seqs, 275673149 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                           BLÓSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ផ្ត	52, Appl	76, Appl	54, Appl	2, Appli	2, Appli	2, Appli	2, Appli	'n	7	74	87, Appl	87, Appl	4, Appli	1, Appli	125, App
	Description	Sequence	Sequence 76,	Sequence 54	Sequence 2, Appl	Sequence	Sequence 2,	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 87,	Sequence 4, Apr	Sequence 1, App	Sequence 125
	ID	US-10-214-932-52	US-10-214-932-76	US-10-214-932-54	US-09-884-681-2	US-09-967-301-2	US-10-457-982-2	US-10-024-686-2	US-10-057-505-2	US-10-293-580-2	US-10-293-580-74	US-09-927-876-87	US-10-360-149-87	US-09-920-922-4	US-09-852-000-1	US-09-900-345A-125
	DB	14	14	14	9	10	12	13	13	14	14	11	15	6	6	10
	Query Match Length DB	545	548	1192	238	238	238	238	238	238	238	387	387	238	238	238
مين	Query Match	98.0	98.0	0.86	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.6	97.6	97.5	97.5	97.5
	Score	1240	1240	1240	1238	1238	1238	1238	1238	1238	1238	1235	1235	1234	1234	1234
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Sequence 2, Appli Sequence 2, Appli Sequence 8, Appli Sequence 10, Appli Sequence 10, Appli Sequence 1159, Appli Sequence 1159, Appli Sequence 1159, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 60, Appli Sequence 60, Appli Sequence 61, Appli Sequence 62, Appli Sequence 64, Appli Sequence 64, Appli Sequence 66, Appli Sequence 66, Appli Sequence 94, Appli Sequence 94, Appli Sequence 100, Appli Sequence 110, Appli Sequence 110, Appli Sequence 110, Appli Sequence 110, Appli Sequence 110, Appli
US-09-866-538-2 US-09-794-308-2 US-09-104-308-2 US-10-132-067-8 US-10-121-258-10 US-10-221-461-6 US-10-305-765-10 US-10-305-765-10 US-10-305-763-110 US-10-305-763-110 US-10-305-763-10 US-10-305-763-10 US-10-305-763-10 US-10-305-765-10 US-09-90-9548-2 US-09-90-9548-3 US-09-90-345A-64 US-09-900-345A-64 US-09-900-345A-68 US-09-900-345A-68 US-10-305-765-98 US-10-305-765-104 US-10-305-765-104 US-10-305-765-110
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ALIGNMENTS

Dy Dies in	Length 545; Indels
SULT 1 Solut 1 Solut 1 Solut 1 Solut 21 Solut 22 Solut 23 Solut 25	98.0%; Score 1240; DB 14; Length 545;
EESULT 1 19-10-214-932-52 Sequence 52, As Publication No GENERAL INFORM APPLICANT: H APPLICANT: H APPLICANT: E TITLE OF INVERITE OF SEQ ID NO 52 LENGTH: 545 TYPE: PRT ORGANISM: AT FREATURE: FREATURE: CURRENT APPLICANT: CURRENT APPLICANT: CURRENT FILIN NUMBER OF SEQ SOFTWARE: PRT CURRENT OF SEQ SOFTWARE: PRT ORGANISM: S45 TYPE: PRT ORGANISM: AT FREATURE: CURRENT APPLICANT: CONTRENT OF SEQ INVERITE OF SEQ INVERITE OF SEQ INVERT CONTRENT OF SEQ INVENT CON	Query Match Best Local Matches 23 27 1 29 1 20 308 20 61 20 368 20 368 20 368

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US-09-884-681-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTISFKDDGNYKTRAEVKFEGDTLV 430
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                        488 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLEFVTAAGITHGMDELYK 545
181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
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Pred. No. 1.2e-123;
1; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                          Sequence 76, Application US/10214932
Publication No. US2003010070741
GENERAL INFORMATION:
APPLICANT: HRANG Inhwan
APPLICANT: LEE, Yong Jik
TITLE OF INVENTION: SYSTEM FOR DETECTING PROTEASE
FILE REFERENCE: APB02/US
CURRENT APPLICATION NUMBER: US/10/214,932
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 133
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 98.0%; Score 1240; DB 14; Best Local Similarity 97.9%; Pred. No. 4e-124; Matches 233; Conservative 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HWANG, Inhwan
APPLICANT: KIM, Dae Heon
APPLICANT: LEE, Yong Jik
TITLE OF INVENTION: SYSTEM FOR DETECTING PROTEASE
FILE REFERENCE: APB02/US
CURRENT APPLICATION NUMBER: US/10/214,932
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 133
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Synthetic Sequence US-10-214-932-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthetic Sequence
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; Sequence 54, Application US/10214932
; Publication No. US20030100707A1
; GENERAL INFORMATION
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Best Local Similarity 97.9
Matches 233; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial FEATURE:
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LENGTH: 1192
                                                                                             RESULT 2
US-10-214-932-76
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LENGTH: 548
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                                        955 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 1014
                                                                                                                                                  1015 VTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTISFKDDGNYKTRAEVKFEGDTLV 1074
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                                                                                                    61 VITIFSKGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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                                                                                                                                                                                                                                                                                                                                                        181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
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MEDIUM TYPE: Floppy disk
COMPUTER: PLOPDY disk
COMPUTER: PLOPPY disk
COMPUTER: PROCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/884,681
FILING DATE: 19-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Assays for Protein Kinases Using
Fluorescent Protein Substrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.9%; Score 1238; DB 9; 97.5%; Pred. No. 2e-124;
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APPLICATION UNDBER: 08/679,865
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Tinear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-884-681-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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ADDRESSEE: Townsend and
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LENGTH: 238 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andrew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tsien, Roger Y.
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STATE: California
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Best Local Similarity 97.5%;
Matches 232; Conservative
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VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 120
                                       121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
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APPLICANT: Myawaki, Atsushi
APPLICANT: Myawaki, Atsushi
APPLICANT: Myawaki, Atsushi
APPLICANT: Remington, S. James
TITLE OF INVENTION: FILORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REPREBNOE: 07257/071001
CURRENT APPLICATION NUMBER: US/10/457,982
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Pred. No. 2e-124;
1; Mismatches 5;
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APPLICANT: Stubbs, Simon L.
APPLICANT: Stubbs, Simon L.
APPLICANT: Stubbs, Anne E.
APPLICANT: Michael, Nigel P.
APPLICANT: Thomas, Nicholas
TITLE OP INVENTION: Fluorescent Proteins
FILE REFERENCE: PA0111
CURRENT APPLICATION NUMBER: US/09/967,301
CURRENT FILING DATE: 2001-09-28
PRIOR FLING DATE: 2001-09-28
PRIOR FLING DATE: 2001-09-28
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2
LENGTH: 238
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PRIOR APPLICATION NUMBER: US/09/602,641
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/172,063
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Publication No. US20030212265A1
GENERAL INFORMATION:
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Best Local Similarity 97.5%;
Matches 232; Conservative
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US-09-967-301-2
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Pred. No. 2e-124;
1; Mismatches 5; Indels 0
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Heim, Roger
TITLE OF INVENTION: MODIFIED GREEN FLUORESCENT PROTEINS
NUMBER OF SQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBHLB FORM:
MEDLIN TYPE: DISKETTE
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: FASCEC for Windlws95
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/024,686 FILING DATE: 17-Dec-2001 PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/057,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: CURRING PARTICULATION DATE: CURRING DATE: 10-OCT-1996
APPLICATION NUMBER: 08/27,452
APPLICATION NUMBER: 08/317,915
FILING DATE: 13-NOV-1995
FILING DATE: 10-NOV-1994
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10024686 Publication No. US20020123113A1 GENERAL INFORMATION:
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Best Local Similarity 97.5%;
Matches 232; Conservative
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                                                                                                                                     TYPE: PRT
ORGANISM: Aequorea victoria
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TYPE: amino acid

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Query Match
Best Local Similarity 97.5%;
Matches 232; Conservative
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US-10-293-580-2
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APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, ROGET
APPLICANT: HSIM, ROGET
APPLICANT: HSIM, ROGET
APPLICANT: CUBITT, Andrew
TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS
FILE REFERENCE: REGENIA60-3
CURRENT APPLICATION NUMBER: US/10/057,505
CURRENT APPLICATION NUMBER: US 08/792,553
PRIOR APPLICATION NUMBER: US 08/792,553
PRIOR APPLICATION NUMBER: US 09/396,003
PRIOR APPLICATION NUMBER: US 09/396,003
PRIOR APPLICATION NUMBER: 1999-09-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PARENTIN DATE: 1999-09-13
SOFTWARE: PARENTIN VERSION 3.1
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Best Local Similarity 97.5%; Pred. No. 2e-124;
Matches 232; Conservative 1; Mismatches 5
TOPOLOGY: linear
MOLECTUR TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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; ORGANISM: Aequorea victoria
US-10-057-505-2
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Sequence 2, Application US/10293580

Sequence 2, Application US/10293580

Sequence 2, Application No. US20030170767A1

Sequence 2, Application No. US20030170767A1

GENERAL INFORMATION: Fluctuation No. US20030170767A1

APPLICANT: Autora Biosciences Corporation
APPLICANT: Autora Fluctuation Number: Valuences Corporation
FILE REFERENCE: August 2002-11-12

CURRENT FILING DATE: 2002-11-12

PRIOR FILING DATE: 1998-07-24

NUMBER OF SEQ ID NOS: 74

SOFTWARE: Patentin version 3.0

SEQ ID NO 2

LENGTH: 238
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Publication No. US20030170767A1
Publication No. US20030170767A1
APPLICANT: Aurora Biosciences Corporation
APPLICANT: Aurora Biosciences Corporation
APPLICANT: Cubit, Andrew B.
TILLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications
FILE REFERENCE: AUROL270 (08366/031001)
CURRENT APPLICATION NUMBER: US/09/129,192
PRIOR APPLICATION NUMBER: US/09/129,192
PRIOR FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn version 3.0
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ORGANISM: Aequorea green fluorescent protein phosphorylation mutant
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Pred. No. 2e-124;
1; Mismatches 5; Indels 0
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151 SKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLV 210
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Pred. No. 5.3e-124;
2; Mismatches 5;
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Patent No. US20020081488A1
GENERAL INFORMATION:
APPLICANT: Miyawaki, Atsushi
CURRENT FILIMG DATE: 2000-08-02
PRIOR APPLICATION NUMBER: UP 2000-237166
PRIOR APPLICATION NUMBER: UP 2000-237166
PRIOR APPLICATION NUMBER: UP 2000-237166
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 238
PRIOR APPLICATION NUMBER: US/09/927,876
PRIOR FILING DATE: 2001-08-10
PRIOR PLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/225,035
PRIOR PLING DATE: 2000-08-11
PRIOR PLING DATE: 2000-08-15
PRIOR PLING DATE: 2000-08-16
NUMBER OF SEC 1D NOS: 107
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 87
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ORGANISM: Artificial Sequence
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US-09-920-922-4
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Matches 232; Conservative
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Best Local Similarity 97.1
Matches 231; Conservative
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                                                                                                                                                                                                                                                                                                      LENGTH: 387
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APPLICANT: Campbell, Robert K
APPLICANT: Campbell, Robert K
APPLICANT: Kelton, Christie A
APPLICANT: He, Chaomei US20040005554Alel Glycoproteins and Methods of Use Thereof
TITLE OF INVENTION: No. US20040005554Alel Glycoproteins and Methods of Use Thereof
FILE REFERENCE: 2093-003
CURRENT APPLICATION NUMBER: US/09/927,876
CURRENT FILING DATE: 2001-08-10
PRIOR PILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 107
SEQ ID NO 87
LENGTH: 387
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APPLICANT: El Tayar, Nabil
APPLICANT: Campbell, Robert K
APPLICANT: Kelton, Christie A
APPLICANT: He, Chaom, Christie A
TITLE OF INVENTION: No. US20030219786Alel Glycoproteins and Methods of Use Thereof
FILE REFERENCE: 20993-003
CURRENT APPLICATION NUMBER: US/10/360,149
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Pred. No. 8.4e-124;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 87, Application US/08927876; Publication No. US20040005554A1; GENERAL INFORMATION:
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Sequence 97, Application US/10360149

; Publication No. US20030219786Al

; GENERAL INFORMATION:
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Best Local Similarity 97.9%;
Matches 232; Conservative 1
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TITLE OF INVENTION: METHOD AND POLYNUCLEOTIDES FOR DETERMINING TRANSLATIONAL
TITLE OF INVENTION: EFFICIENCY OF A CODON
FILE REFERENCE: 10338-5US
CURRENT APPLICATION NUMBER: US/09/900,345A
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: M PP8078
PRIOR FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: PCT/AU00/00008
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121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
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                                                                                   1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Osumi, Takashi
APPLICANT: Osumi, Takashi
APPLICANT: TSUKAmeto, Toshiro
APPLICANT: TSUKAmeto, Toshiro
APPLICANT: TSUKAmeto, No. US20020099170Aliyo
APPLICANT: TSUKAmeto, No. US20020099170Aliyo
APPLICANT: Yamasaki, Masatoshi
TITLE OF INVENTION: GREEN FLORESCENT PROTEINS AND BLUE FLUORESCENT
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: 046124-5005-US
CURRENT APPLICATION NUMBER: US/09/852,000
CURRENT APPLICATION NUMBER: US 09/121,539
PRIOR FILING DATE: 1998-01-23
PRIOR FILING DATE: 1998-07-24
PRIOR FILING DATE: 2000-07-13
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97.5%; Score 1234; DB 9; Length 238;
Best Local Similarity 97.1%; Pred. No. 5.3e-124;
Matches 231; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ), OTHER INFORMATION: Green fluorescent protein US-09-852-000-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 125, Application US/09900345A Publication No. US20030031999A1 GENERAL INFORMATION:
APPLICANT: Frazer, lan Hector APPLICANT: Zhou, Jian
                                                                                                                                                                                                                                Sequence 1, Application US/09852000 Patent No. US20020099170A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Aequorea victoria
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SOFTWARE: Patentin Ver. 2.0
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US-09-900-345A-125
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LENGTH: 238
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US-09-852-000-1
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                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                          FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: GFP humanized
OTHER INFORMATION: control
US-09-900-345A-125
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0
                                                                                                                                                                                                                                                                                              Length 238;
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                           Score 1234; DB 10;
Pred. No. 5.3e-124;
2; Mismatches 5;
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Job time : 47 secs
                                                                                                                                                                                                                                                                                                 97.58;
97.18;
                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 185
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 125
LENGTH: 238
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 97.1
Matches 231; Conservative
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